E v o l D i r

September 1, 2003

M o n t h i n R e v i e w

Forward

This listing is intended to aid researchers in population genetics and evolution. To add your name to the directory listing, to change anything regarding this listing or to complain please send me mail at Golding@McMaster.CA.

Listing in this directory is neither limited nor censored and is solely to help scientists reach other members in the same field and to serve as a means of communication. Please do not add to the junk e-mail unless necessary. The nature of the messages should be "bulletin board" in nature, if there is a "discussion" style topic that you would like to post please send it to the USENET discussion groups.

Instructions for the EvolDir are listed at the end of this message.

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Conferences

ShizuokaU DynamicSystems Mar14-17

announcement (free to distribute) International Symposium on Dynamical Systems Theory and Its Applications to Biology and Environmental Sciences

March 14-17, 2004 in Shizuoka University

Symposium Objectives The purpose of "The International Symposium on Dynamical Systems Theory and Its Applications to Biology and Environmental Sciences" is to discuss many interests on the rich properties of dynamical systems appeared in biology and environmental sciences. The symposium constitutes of the lectures by about 30 eminent mathematical biologists and contributed oral or poster sessions. Asian contributors are especially welcome to the symposium...(full PDF document click here)

Collections of papers based on the presentations made during the symposium may appear as special issues of international journals and as a book from Springer-Verlag. We already have agreements with Ecological Modeling and J. Comput. Appl. Math and Mathematical Biosciences.

Scientific Committee

Chair (K. Sigmund: University of Vienna), Co-chair (Y. Takeuchi: Shizuoka University)

members: M. Mimura (Hiroshima University), N. Shigesada (Nara Women's University), T. Hara (Osaka Prefecture University), T. Furumochi (Shimane University), T. Namba (Osaka Women's University), Y. Iwasa (Kyushu University), T. Kajiwara (Okayama University), H. Inaba (University of Tokyo), T. Sasaki (Okayama University),

Organizing Committee (Shizuoka University)

General Chair (Y. Takeuchi), Local Chair (K. Tainaka, T. Oohara), Program Chair : K. Sato, R. Miyazaki, T. Hasegawa (WEB), M. Nakamaru (Abstract) Registration Chair : S. Morita, R. Kon, Y. Saito Liaisons: J. Yoshimura, members: K. Ashizawa, N. Ooba

Correspondence takeuchi@sys.eng.shizuoka.ac.jp Yasuhiro Takeuchi, Faculty of Engineering, Shizuoka University 3-5-1 Johoku, Hamamatsu, Shizuoka, 432-8561, JAPAN. tel: +81-53-478-1200

this announcement sent by jin yoshimura, professor Faculty of Engineering, Shizuoka University 3-5-1 Johoku, Hamamatsu, Shizuoka, 432-8561, JAPAN.

Jin Yoshimura <jin@sys.eng.shizuoka.ac.jp>

ShizuokaU DynamicSystems Mar14-17 2

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Jin Yoshimura <jin@sys.eng.shizuoka.ac.jp>

UConnecticut NEMEB Nov1

CALL FOR ABSTRACTS

The 14th Annual New England Molecular Evolutionary Biologists Meeting

Invited Speakers:

Dr. Laura Katz, Dept of Biological Sciences, Smith College

Dr. Michael O'Neill, Dept of Molecular and Cell Biology, University of Connecticut

Dr. Timothy Shank, Dept of Biology, Woods Hole Oceanographic Institution

Dr. John Wakeley, Dept of Organismic & Evolutionary Biology, Harvard University

Saturday, November 1, 2003

University of Connecticut Storrs Campus

Building BSP Room 131 N. Eagleville Road Storrs, CT

Contact Dr. Rachel O'Neill email: roneill@uconnvm.uconn.edu

Registration: http://www.mcb.uconn.edu/-nemeb2003/index.html Registration Deadline: October 10, 2003

Registration Fee: FREE!

We are looking forward to your participation in this FREE one-day regional meeting! NEMEB is a forum for principal investigators as well as post-doctoral and graduate students to present their work and to interact with one another about their exciting work in the field of molecular evolutionary biology. The meeting format consists of a combination of invited presentations by established faculty members, contributed talks from attendees and a poster session.

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Olga A. Zhaxybayeva Department of Molecular and Cell Biology University of Connecticut Biology/Physics Building Room 426, Unit 3125, 91 North Eagleville Road Storrs CT 06269-3125

Tel: (860) 486-1887 (lab) Fax: (860) 486-4331 Email: olga.zh@uconn.edu Web: http://www.sp.uconn.edu/-˜oaz98001/ Mirror: http://carrot.mcb.uconn.edu/˜olgazh

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UHertfordshire Evolvability Aug26-28

Call-for-Papers and Participation

Symposium on

"Evolvability, Genetics & Development in Natural and Constructed Systems"

sponsored by:

EPSRC Network on Evolvability in Biological and Software Systems University of Hertfordshire, U.K. University College London, U.K.

Tewin Bury Farm Hotel, Hertfordshire England, UK 26-28 August 2003

[about 30 minutes north of London by train and taxi from the Welwyn Garden City station; accessible from Heathrow and other London area airports; nearest airport London Luton]

SCOPE

This symposium will serve as a forum to explore the current state of knowledge on the evolvability of genetic regulatory networks in development for both biological and artificial systems.

26 August: Arrival day, Welcome reception

27-28 August: Lectures and discussion (two full-days)

[29 August a.m.: Departure for guests staying on-site]

Speakers (Confirmed):

* Hans Meinhardt (Max-Planck-Institute for Developmental Biology)

* Michael Frohlich (Natural History Museum, London)

* Chrystopher L. Nehaniv (University of Herfordshire)

* Peter J. Bentley (University College London)

* Julian Miller (University of Birmingham)

* Sanjeev Kumar (University College London)

* Tom Quick (University College London)

Speakers (To Be Confirmed):

* Gunter P. Wagner (Yale University) * Paulien Hogeweg (University of Utrecht) * Maria Schilstra (University of Hertfordshire, BioComputation) * Josh Bongard (Cornell University & Univ. Zurich) * Olivier Pourquie (Stowers Institute for Medical Research) * R. Scott Poethig (University of Pennsylvania) * Gregory S. Hornby (NASA Ames Research) * Wallace Arthur (University of Sunderland) * Lee Altenberg (University of Hawaii) * Paul Marrow (British Telecom) * Richard Tateson (British Telecom) * Thomas S. Ray (ATR Japan & University of Oklahoma) * Wolfgang Banzhaf (University of Dortmund) * John R. Koza (Stanford) * Irina Abnizova (University of Hertfordshire, BioComputation) * Attila Egri-Nagy (University of Hertfordshire, Algorithms) * Christophe Battail (University of Hertfordshire, BioComputation)

Program Committee:

Chrystopher L. Nehaniv University of Hertfordshire, U.K. (Director, EPSRC Network on Evolvability in Biological & Software Systems)

Peter J. Bentley and Sanjeev Kumar University College London, U.K. (Editors of the book "On Growth, Form and Computers")

PARTICIPATION, SUPPORT, & SUBMISSIONS OF CONTRIBUTED TALKS AND POSTERS:

Subject to limitations on space, attendance is open to members of the scientific community working in relevant areas including postgraduate students. Prospective participants should email C.L.Nehaniv@herts.ac.uk to register. Some time will be available for contributed talks and possibly posters. Abstracts may be submitted C.L.Nehaniv@herts.ac.uk in plain text via email. Lunch and refreshments are provided for day delegates, and dinner can be arranged. Full or partial support will will be available for Evolvability Network members and UK-based postgraduate students presenting a paper or poster. Please contact C.L.Nehaniv@herts.ac.uk to inquire about support.

c.l.nehaniv@herts.ac.uk

UMontpellier EvolHumanBiol Dec1-3

Human Biology: an evolutionary perspective

University of Montpellier II, France December 1-2-3, 2003

Website and call for presentations: http://-/www.isem.univ-montp2.fr/GE/meeting_site/-human_biology.htm

Purpose and scope: Evolutionary biology is now invading new territories, and numerous scientific areas are experiencing breakthroughs due to reconsideration in an evolutionary perspective... This is particularly true for the scientific study of man : sociology, anthropology, ethnology, medicine, physiology, dietetics, psychiatry, economics, law, politics, theology, etc.

What has been achieved so far is probably just the tip of the iceberg, and a major change in the understanding of

ourselves and of our social world is probably underway.

This workshop is dedicated to present an up to date overview of some of these revisited human topics. It is particularly devoted to scientists and graduate students already familiar with evolutionary biology. It is also addressed to everyone interested by stimulating ideas on human biology and ecology, which are based on firm scientific grounds (Darwinian evolution).

Michel Raymond <raymond@isem.univ-montp2.fr>

UWollongong 3rdAustEvol Feb10-12

Dear Evolutionary Biologists,

The University of Wollongong, NSW Australia, is hosting the 3rd Australasian Evolution Meeting. It will be held from Tuesday 10th to Thursday 12th February 2004. Presentations on all aspects of evolutionary biology are welcome.

We are encouraging both staff and students to present in an informal and relaxed environment. At this stage we expect the meeting will run as a single session over 2 days, and will cost about AU$250 for full, and AU$120 for student registration (which includes the mixer on Tuesday10th February, lunches and an informal conference dinner).

Additional information can be found on the preliminary conference web site: (check this site regularly for updates)

http://www.uow.edu.au/science/biol/aes2004 To enable us to plan for the conference and to finalise costs we need a better estimate of the number of participants. If you are interested in attending please reply to Julie Wright via juliew@uow.edu.au with your name, research group and institution, indicating;

- if you are a staff or student - whether you plan to attend or present (what format - poster/slides/PowerPoint) - whether you will require accommodation (preferred option - caravan park/campus/hotel), - how many people from your group are likely to participate.

We look forward to hearing from you.

Regards,

Paul Rymer and Tanya Strevens For AES Organizing Committee ..... Paul Rymer Institute for Conservation Biology University of Wollongong NSW 2522 Australia

Phone (61) 2 4221 4266 Fax (61) 2 4221 4135 pdr01@uow.edu.au

Paul Rymer <pdr01@uow.edu.au>

Valencia MEEGID Jul19-23

07/08/03

The 7th International Meeting "Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases" (MEEGID VII) will be held in Valencia (http://-/www.valencia-on-line.com/), Spain, 19th-23rd July 2004. As for the 6 first MEEGID meetings, it will be co-organized by the Centers for Disease Control and Prevention (CDC; http://www.cdc.gov/) in Atlanta, the Centre National de la Recherche Scientifique (CNRS; http://www.cnrs.fr/) and the Institut de Recheche pour le Développement (IRD; http://-www.ird.fr/) in France.

MEEGID VII will be hosted by the 9th European Multicolloquium of Parasitology (EMOP IX; http://-www.uv.es/emop9/). Several sessions will be organized in common by the 2 meetings.

The MEEGID meetings are organized in synergy with the new journal Infection, Genetics and Evolution (Elsevier; http://www.elsevier.nl/locate/meegid), which scientific topic is identical to that of the MEEGID. Launched less than 2 years ago, Infection, Genetics and Evolution is now published with 6 issues per year, and is covered by Medline and Index Medicus, starting from the 1st issue.

Communications on genetics, genomics, proteomics, population biology, mathematical modelling, bioinformatics are welcome. They can deal with the host, the pathogen or the vector. Papers considering host + pathogen or pathogen + vector (co-evolution) are particularly encouraged. All pathogens are within the scope of MEEGID: viruses, parasitic protozoa, helminths, fungal organisms, prion. All infectious models can be considered, including those of veterinary or agronomical relevance.

The papers communicated for MEEGID VII will be published in a special issue of Infection, Genetics and Evolution, as already done for MEEGID VI (Paris, July 2002). MEEGID VII will include 10-15 plenary lectures, about 20 specialized symposia, 12-15 "express-

debates" (20 mn presentation by only one speaker followed by 40 mn free discussion) and several poster sessions.

Awards will be attributed to the best communication, the best communication by a student and the best communication by a scientist from the Southern World on a problem specifically relevant to these areas.

Organizers:

Michel Tibayrenc Editor -in-chief Infection, Genetics and Evolution (Elsevier) http://www.elsevier.nl/-locate/meegid President Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID) Society Director Unit of Research "Genetics and Evolution of Infectious Diseases" UMR CNRS/IRD 9926 IRD, BP 64501 34394 Montpellier cedex 5, France Email Michel.Tibayrenc@mpl.ird.fr Website http://cepm.mpl.ird.fr Santiago Mas Coma Organizer EMOP IX Departamento de Parasitologia Facultad de Farmacia, Universidad de Valencia Av. Vicent Andrés Estellés s/n 46100 Burjassot-Valencia, Spain Email S.Mas.Coma@uv.es

Altaf lal Chief, Molecular Vaccine Section Division of Parasitic Disease National Center for Infectious Diseases Centers for Disease Control and Prevention Mail Stop F-12 4770 Buford Hwy.NE Chamblee, Atlanta GA 30341-3724, USA Email aal1@cdc.gov

Abstract submission deadline: April 30th 2004. Please follow format of Infection, Genetics and Evolution (Elsevier; http://www.elsevier.nl/locate/meegid) for names of authors and litterature cited, about 1/2 page, by email. Abstract must include complete address, phone, fax and email numbers of the corresponding author. Please send a final version. Corrections will not be accepted.

Michel.Tibayrenc@mpl.ird.fr

Virginia ConsGenet Sep14-17 3

Please join us for the Inaugural Conservation Genetics Conference of the American Genetic Association on September 14-17, 2003 in Front Royal, Virginia. We have an exciting agenda and list of speakers and participants including: Fred Allendorf, Scott Baker, Keith Crandall, Robert DeSalle, Robert Fleischer, James Hamrick, Gordon Luikart, Philip Morin, Craig Moritz, Stephen O'Brien, Stephen Palumbi, Howard Rosenbaum, Oliver Ryder, Barbara Schaal, Lisette Waites and Robert Wayne.

We are still accepting applications for poster presentations.

For further information and the full agenda, please visit our website:

http://congen2003.ncifcrf.gov/

Email: Congen2003@ncifcrf.gov Website: http://-congen2003.ncifcrf.gov/

Al Roca <roca@ncifcrf.gov>

Virginia SEEPAGE Sept19-21 3

SEEPAGE (South-East Ecology, PopulAtion Genetics and Evolution) meeting registration deadline has been extended until August 31. Late registration fee will apply after that date. We also have precious few slots left in the program. If you are planning to attend and have not registered yet, please do it as soon as possible. Details on the web page: http://faculty.etsu.edu/-yampolsk/SEEPAGE2003/ Please contact me if you have any questions.

Lev Yampolsky

Department of Biological Sciences East Tennessee State University Johnson City TN 37614-1710 Phone 423-439-4359 Fax 423-439-5958 yampolsk@mail.etsu.edu

WageningenNL PARTNER Nov19-23

Final announcement: Call for Expressions of Interest for PARTNER-1, Nov. 2003

A first Workshop in a series of four on the Ecology and Evolution of Asexual Reproduction

Wageningen, The Netherlands, November 19-23, 2003

The PARThenogenesis NEtwoRk (PARTNER) is a network on the ecology and evolution of asexual reproduction, funded by the European Science Foundation (ESF, http://www.esf.org/).

The First Workshop is about Asexuality and Time-

scales and includes: (1) ancient asexuals (2) ancient asexual genes (3) methods of ageing in asexuals (4) pests in agriculture

For more information see: http://www.nioo.knaw.nl/-NETWORKS/PARTNER Confirmed speakers are: Bengt O. Bengtsson, Sweden C. W. (Bill) Birky Jr., Tucson, USA Michael Heethoff, Germany Hugh D. Loxdale, England David Mark Welch, Woods Hole, USA Koen Martens, Belgium Matthew Meselson, Cambridge, USA Claudia Ricci, Italy W. L. (Bill) Rice, Santa Barbara, USA Ian Sanders, Switzerland Isa Schon, Belgium Tim Sharbel, France Peter Van Dijk, The Netherlands

Submission deadline is August 15th, 2003

Expression of interest: Please send an expression of interest with a brief CV, and a maximum of one page summary with your thoughts about what you can gain from and contribute to the workshop. Students are also invited to apply. The number of participants is limited. In case of approval, you will be invited to participate. Meals and accommodation will be provided by the ESF. Travel costs will NOT be reimbursed

For more information and submission of expression of interest for the first workshop, please contact:

Kitty Vijverberg Netherlands institute of Ecology PO Box 40 NL-6666 ZG Heteren The Netherlands k.vijverberg@nioo.knaw.nl

GradStudentPositions

UCanterburyNZ EvolGenomics

Ph.D. Scholarships Available in Evolutionary Genomics at the University of Canterbury, Christchurch, New Zealand.

We are currently seeking up to 3 students with interests in genomics, evolution and bioinformatics to conduct research on microsatellite evolution. Positions are available immediately for a period of 3 years.

Project Description Microsatellites are abundant, highly variable, repeated DNA sequences that are regarded as the most versatile genetic markers yet discovered. They are the cornerstone of the current biological revolution and are used in gene mapping, DNA forensic work, and as population markers. Conclusions drawn from such studies in many cases depend critically on assumptions about how microsatellites evolve. Current models of microsatellite evolution are overly simplistic and almost certainly incorrect, leading to widespread data misinterpretation. To avoid continued misinterpretation, it is vital that we understand fully how microsatellites evolve. This project will investigate the processes governing microsatellite evolution by comparing microsatellite sequences derived from the human, mouse, rat and other genome projects using a combination of bioinformatics and comparative molecular genetics.

The Ideal Candidate The ideal candidate will possess experience in both molecular genetics and bioinformatics. They will be motivated and organised, with a demonstrated capacity to master the broad skill set necessary for the successful completion of a research program that will span molecular genetics, bioinformatics and biomathematics. They will be a competent laboratory worker, with experience of all routine molecular genetic techniques, particularly microsatellite genotyping and sequencing, and should be computer literate with familiarity with database management and statistical analyses. Minimum qualifications: B.Sc. (Hons),

M.Sc. in Genetics, Molecular Biology or equivalent.

Remuneration Students will receive an annual stipend of NZ$19,000 plus local fees for 3 years. Please note that students from countries other than New Zealand, Germany, France, and Australia will normally be required to pay international fees currently NZ$23,000 per annum which will not be covered by the stipend. Additional scholarships for international fees are available, but only to the very best international graduates.

Interested applicants are encouraged to make informal enquires to Dr. Neil Gemmell, in the first instance. To apply, please send your Curriculum Vitae, a copy of your academic transcript and the names of three referees with a covering letter to:

Dr. Neil J Gemmell Senior Lecturer in Molecular Genetics School of Biological Sciences, University of Canterbury Private Bag 4800, Christchurch, New Zealand Phone: +64 3 364 2009 Fax: +64 3 364 2590 e-mail: neil.gemmell@canterbury.ac.nz http://-www.biol.canterbury.ac.nz

UHelsinki StatGenet

UNIVERSITY OF HELSINKI ROLF NEVANLINNA INSTITUTE Res Inst Math, Stat & Comp Sci

3-year PhD student position in Statistical Genetics.

This position is available to work with Mikko J. Sillanpää on the development of statistical methods to combine information from several sources into a single large probabilistic gene mapping analysis. Information sources considered in the statistical analysis are genomic information provided by large sequencing projects (e.g. Human Genome Project), phenotypic trait measurements, multilocus markers, and gene expression microarrays. Probabilistic Bayesian inferential machinery will be adopted for modeling and analytic purposes. An algorithmic Markov Chain Monte Carlo simulation is utilized in numerical implementation. The developed new methods are put publicly available on the net as software packages.

The department has a strong competence in statistical genetics and is a member of the Centre of Population Genetic Analyses (Center of Excellence of the Academy of Finland 2002-2007).

The applicant should have a MSc-degree either in Statistics, Genetics or Computer Science. Applicants should send a copy of a CV and contact information of two referees. The position is open until a suitable candidate has been found.

email: mjs@rolf.helsinki.fi homepage: http://-www.rni.helsinki.fi/~mjs) fax: +358-9-191-22779

Mikko Sillanpaa <mjs@rni.helsinki.fi>

UMaine GuppyGeneFlow

A graduate studentship is immediately available in the study of natural selection, gene flow and adaptation in the wild. In particular, this research will focus on interactions between gene flow and selection in constraining the adaptation of populations of Trinidadian guppies (Poecilia reticulata). This work will involve extensive field studies in Trinidad, including opportunities for experimental manipulations in the wild. The successful candidate will also likely participate in developing complimentary molecular, modeling and laboratory experiment approaches. This work will occur in collaboration with cooperating investigators from McGill University (Dr. Andrew Hendry), the University of California, Riverside (Dr. David Reznick) and Dalhousie University (Dr. Paul Bentzen).

Candidates interested in this NSF funded position must be prepared to work in (at times) remote locations and a foreign culture. This studentship provides tuition, salary and research support. Applicants pursuing PhD degrees are preferred, particularly those with prior MS degrees or research experience. However, other highly qualified students will be considered. Though this graduate position is immediately available, start dates may be negotiable.

Interested Candidates should contact:

Dr. Michael T. Kinnison

Department of Biological Sciences

321 Murray Hall

University of Maine

Orono, ME 04469.

E-mail: michael.kinnison@umit.maine.edu

Phone: 207-581-2575

Interested candidates should send inquiries and supporting materials vial e-mail. If possible, supporting materials should include a CV, standardized test scores

(GREs), indication of prior course work (preferably with grades), and contact information for recommendations. Ultimately, competitive candidates will be asked to submit formal application materials for graduate study at the University of Maine (Biological Sciences or Ecology and Environmental Sciences Programs). Review of applicants will begin immediately and continue until an acceptable candidate is determined.

Michael T. Kinnison Phone: 207-581-2575 Assistant Professor Fax: 207-581-2537 Department of Biological Sciences E-mail: michael.kinnison@umit.maine.edu 321 Murray Hall, University of Maine Orono, ME 04469

Warwickshire RareBreeds

The Rare Breeds Survival Trust has a national role to promote and conserve rare and threatened breeds of farm livestock within the UK. The Trust currently supports over 70 breeds of cattle, goats, horses, ponies, pigs, poultry and sheep.

A vacancy has now arisen for a temporary, fixed term position as full time Assistant to the Trust's Technical Adviser.

The successful candidate, who will have a good honours degree in biology, preferably with training or postgraduate experience in population genetics, will take forward a number of projects relating to the conservation of rare breeds of farm animals. He/she will possess sound analytical and IT skills, initiative and experience in report writing and communication. .

The post holder will be based at the Trust's office at Stoneleigh Park, Kenilworth, Warwickshire and the six-month, fixed term contract will attract a salary up to £1,550 per month. In addition, any travel = expenses incurred during the course of the contract will be met.

The closing date for receipt of applications is Friday 22 August 2003. Please send your application, with CV by email to Karen Anderson, who can provide a more detailed job description on request. (email: karen@rbst.org.uk or telephone: 024 76 69 6551).

rosemary.mansbridge@rbst.org.uk rosemary.mansbridge@rbst.org.uk

Jobs

AthensGeorgia ResTech

A full-time research technician position is available immediately in the USDA Agricultural Research Service in Athens, Georgia. The job will be funded by a grant to study the molecular epidemiology of a food-borne pathogen, Campylobacter jejuni, among poultry oper-

ations in Iceland. Job duties will include microbial culture, PCR, preparation of isolates for sequencing, and the maintenance of some laboratory equipment.

The ideal candidate will have some experience in biological research. This job may be ideal for recent graduates who are considering further graduate or medical education. Salary will be dependent on qualifications (ranging from $22, 948 to $28, 644 per year), and benefits will be included. A complete description of the job and instructions for application are available at <http://www.afm.ars.usda.gov/divisions/-hrd/vacancy/D3S-3264.htm> .Applications will be accepted through August 18, 2004.

Kenneth Callicott kcallicott@saa.ars.usda.gov

Edinburgh EcolGenetics

Ecological Geneticist CEH Edinburgh

The Centre for Ecology and Hydrology (CEH), part of the Natural Environment Research Council (NERC) carries out large-scale and long-term research in the terrestrial and freshwater sciences to support a broad user community. We address key environmental issues through integrated monitoring, process studies and predictive modelling, and the development of essential infrastructure and facilities.

We require an enthusiastic scientist to work as part of a team on projects that are evaluating genetic diversity in tropical and temperate trees. The work will be lab-based, conducting DNA extractions, optimising PCR procedures and performing micro-satellite and AFLP analysis. Most of the collections have already been made but we would expect you to be willing to make further collections in the UK or overseas if required.

You will require a first degree or equivalent in a relevant subject. Good molecular genetic lab skills and record keeping are essential. Experience in data-basing would be a distinct advantage, and familiarity with genetic data analysis tools an added bonus.

The salary is £16,010 progressing to £18,750 per annum. In addition NERC offer a pension scheme, 25 days' annual leave and $10\frac{1}{2}$ days' public and privilege holiday. The appointment will be for a fixed term of 2 years to cover a temporary secondment.

For further details and an application form, please write to Hannah Moore, Admin HQ, CEH Monks Wood, Abbots Ripton, Huntingdon, Cambs PE28 2LS or E-mail: hajm@ceh.ac.uk quoting the reference number CEH HQ 120.

The closing date for receipt of completed applications is 11 September 2003.

The Council has an equal opportunities policy and welcomes applications from all sections of the community. People with disabilities and those from ethnic minorities are currently under-represented and their applications are particularly welcome. Many parts of NERC operate a guaranteed interview scheme for suitable applicants with disabilities.

HarvardMedSchool ResTech

HARVARD MEDICAL SCHOOL DEPARTMENT OF GENETICS

Advertisement for a Research Technician

Job description: (1) Carrying out large-scale genotyping and sequencing to analyze human and primate genetic variation, searching for clues about the positions of disease genes and important events in human and hominid evolution. (2) Data quality control and analysis of large-scale data sets (3) Helping to set up a laboratory for medical and population genetics. This includes making sure equipment operates properly, and ordering reagents and materials.

Desired background: A master's degree or at least two years of post-college research experience in population genetics or molecular evolution. The successful candidate will be familiar with PCR, and expert in DNA sequencing or genotyping. Familiarity with bioinformatics tools is essential, and a background in statistics and PERL programming is important. The work will involve quality control of genomic-scale data sets in Excel and other computer programs, and so the successful applicant will be comfortable with these software tools.

Salary: $32,000-$37,000 per year Expected time commitment: at least 3 years Start date: between November 1, 2003 and January 4, 2004

A cover letter explaining your interest in this position, and a curriculum vitae (C.V.), should be sent to Linda Musto, Harvard Medical School 25 Shattuck St, Gordon Hall 010, Office of Human Resources, Boston, MA 02115 quoting reference number 16940, or e-mail linda_musto@hms.harvard.edu. We will contact you if

we feel that there is a good match. The closing date for applications is Friday, August 22, 2003.

Many thanks,

David Reich

David Reich <reich@genome.wi.mit.edu>

IndianaU GenomicsBioinformatics

PhD-level Research Scientists The Center for Genomics and Bioinformatics Indiana University, Bloomington

The Center for Genomics and Bioinformatics at Indiana University, Bloomington, carries out research in functional genomics and bioinformatics, working both autonomously and in collaboration with faculty. The CGB is expanding to create a new NIH-funded Drosophila Genomics Resource Center (DGRC) that will produce research materials and carry out exploratory studies on behalf of the Drosophila research community nationally.

In connection with the DGRC, the CGB has immediate openings for several Ph.D. scientists. Successful applicants will join other CGB scientists in research projects bearing on microarray production, microarray data analysis, laser capture microdissection, RNA amplification, fluorescent DNA labeling technologies, vector design, and cell culture methods. Candidates should have a Ph.D. and research experience in one or more of the following areas: molecular biology, cell culture, functional genomics, or computational biology. Candidates with prior experience in microarray methods are especially encouraged to apply.

The CGB is a growing research center that is part of an active and expanding research community in the life sciences. Visit our website (http://cgb.indiana.edu) to see our ongoing activities and collaborations.

Both positions are open now and applications will be accepted until the positions are filled. Those received by September 1 will be assured full consideration.

Please submit a cv and a description of your background and interests, and arrange that 3 letters of recommendation be sent directly to: Genomics Search, Center for Genomics and Bioinformatics, Indiana University, 1001 E. 3rd St., Bloomington, IN 47405-3700. Indiana University is an affirmative action equal opportunity employer.

Jennifer Steinbachs, Ph.D. Deputy Director The Center for Genomics and Bioinformatics Indiana University Jordan Hall Bloomington, IN 47405-3700 voice 812.856.1858 fax 812.856.9340 http://cgb.indiana.edu

IndianaU MicrobialEvol

MICROBIAL ECOLOGIST/EVOLUTIONARY BIOLOGIST Department of Biology Indiana University, Bloomington

The Department of Biology invites applications for a tenure-track Assistant Professor working in microbial ecology/evolutionary biology. We seek candidates with interests and backgrounds in experimental and/or theoretical approaches to microbial ecology and evolution who will complement recent hires in the areas of microbiology, molecular evolution, and community ecology. We are especially interested in candidates investigating the function of microbes in natural systems, and we define microbes broadly to include viruses, prokaryotes, fungi and protists.

The successful candidate will be provided with a competitive start-up package and will be expected to establish a vigorous externally funded research program and to participate in teaching undergraduate and graduate courses. For information about the Biology Department and for links to the campus and the Bloomington community, see http://www.bio.indiana.edu . Candidates should send a curriculum vitae, a statement of research, and representative publications, and arrange to have three (or more) letters of recommendation sent to: Curt Lively, Microbial Ecology/Evolution Search, Department of Biology, Indiana University,1001 E. Third Street, Bloomington, IN 47405-3700. Review of applications will begin October 7, and will continue until suitable candidates are identified.

Indiana University is an Affirmative Action/Equal Opportunity Employer. Women and minority candidates are encouraged to apply.

curt lively <clively@indiana.edu>

IndianaU Tech GenomicsBioinformatics

Positions for Research Associates/Technicians The Center for Genomics and Bioinformatics Indiana University, Bloomington

The Center for Genomics and Bioinformatics at Indiana University, Bloomington, carries out research in functional genomics and bioinformatics, working both autonomously and in collaboration with faculty. The CGB is expanding to create a new NIH-funded Drosophila Genomics Resource Center (DGRC) that will produce research materials and carry out exploratory studies on behalf of the Drosophila research community nationally.

In connection with the DGRC, the CGB has immediate openings for several technical staff. Successful applicants will assist CGB scientists in producing, testing, and distributing DNA microarrays, maintaining and distributing an important archive of DNA molecules, and growing and distributing cell lines. They will also assist in research projects associated with these efforts.

The ideal candidate will have a B.S. or M.S. in Biology or Biochemistry and some laboratory experience in molecular biology, cell biology, or genomics. However, candidates with degrees in other scientific fields will be considered. Given a good scientific background, enthusiasm, interest in the projects, and reliability will weigh more heavily than the field of the degree.

The CGB is a growing research center that is part of an active and expanding research community in the life sciences. Seee our website (http://cgb.indiana.edu) for more details about our ongoing activities and collaborations.

Both positions are open now and applications will be accepted until the positions are filled. Those received by September 1 will be assured full consideration.

Please submit a cv and a description of your background and interests, and arrange that 3 letters of recommendation be sent directly to: Genomics Search, Center for Genomics and Bioinformatics, Indiana University, 1001 E. 3rd St., Bloomington, IN 47405-3700. Indiana University is an affirmative action equal opportunity employer.

Jennifer Steinbachs, Ph.D. Deputy Director The Center for Genomics and Bioinformatics Indiana University Jordan Hall Bloomington, IN 47405-3700 voice 812.856.1858 fax 812.856.9340 http://cgb.indiana.edu

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Madison MaizeGenome

Molecular and Functional Diversity in the Maize Genome Project Manager

We invite applications for the position of project manager for a multi-institutional NSF Plant Genome Project. The project has two foci: (1) analysis of molecular diversity in the genomes of maize and its wild relatives by SNP genotyping with the principal goals of testing several thousand genes for evidence of selection during maize domestication and improvement and better understanding how historical and demographic factors have shaped the maize genome, and (2) testing diverse alleles at one thousand candidate genes for functional variation on agronomically and evolutionarily important phenotypes through a combination of high-throughput linkage and association mapping.

Members of the project include Ed Buckler (USDA/ARS and Cornell University), John Doebley (University of Wisconsin), Brandon Gaut (UC-Irvine), Major Goodman (North Carolina State University), James Holland (USDA/ARS and North Carolina State University), Steve Kresovich (Cornell University), Mike McMullen (USDA/ARS and University of Missouri), Lincoln Stein (Cold Spring Harbor Lab) and Doreen Ware (USDA/ARS and Cold Spring Harbor Lab).

The project manager will have diverse responsibilities related to coordinating activities among the different project groups, working with our informatics group, presenting project accomplishments at national meetings, and reporting project results to the National Science Foundation. The project manager will also have opportunity to participate in data analysis and publication. The position is available January 1, 2004, is funded for five years, and will be located in Madison, Wisconsin.

Applicants should have a Ph.D. in the biological sciences with training in either evolution, agronomy, plant biology, genetics, population genetics or related area. We specifically seek individuals with some background or interest in developing expertise in informat-

ics. Strong organizational and communication skills are required. Applications (including a cover letter, CV, publication pdf files, and names, phone numbers and email addresses of three references) and inquiries should be directed by email to John Doebley, Department of Genetics, University of Wisconsin, jdoebley@wisc.edu.

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NewportOR MolGenetTech

Dear Evoldir Colleagues-

Please pass on this message to any students and/or colleagues who might be interested in the position.

I am seeking to hire a full-time permanent laboratory technician to conduct research in the areas of quantitative and molecular genetics of shellfish, especially oysters. The position is with the USDA Agricultural Research Service as part of a program for the selective breeding of cultured shellfish (http://www.ars.usda.gov/research/projects/-projects.htm?ACCN_NO@5577&fy 02) . The position is located in Newport, OR at Oregon State University's Hatfield Marine Science Center (http://-hmsc.oregonstate.edu/). The laboratory is designed for high-throughput genotyping of microsatellite and single-nucleotide polymorphisms, including automated DNA sequencing and liquid handling, and research will focus on using these methods for QTL mapping and gene expression analyses of loci contributing to life history traits , stress and disease resistance, economically important characters such as shelf-life and meat quality, and morphological characters such as shell shape and coloration patterns. Recently, a larger number of mapped microsatellite loci have become available in the Pacific Oyster, Crassostrea gigas, that will greatly facilitate this work, and SNP markers are in development in other laboratories. In addition the main campus in Corvallis has the technology for microarray analysis, and there is a growing amount of sequence data available will greatly facilitate the development of DNA chip technology in the near future.

The ideal candidate would have a Master's degree, but practical experience in a working lab would be considered equivalent if it provided familiarity with the necessary molecular techniques (DNA/RNA isolation, PCR, electrophoresis, molecular cloning, DNA sequencing etc.). Familiarity with the bioinformatic and statistical approaches used to analyze molecular genetic data are also highly desirable , but training can be provided. There will be some field work required for animal rearing and data collection. I am looking for more of a high-level laboratory manager who will contribute to the intellectual aspects of the work rather than simply a pair of hands at the bench. There will be ample scope for independent projects, presentation of results at meetings and in publications, and participation in formulating research agendas. The advertised salary range is large, so there is ample scope for advancement for more junior applicants, and more senior applicants will be given full consideration.

Newport is a small, oceanfront city with unspoiled beaches, an active fishing fleet, and numerous tourist attractions located at the mouth of the Yaquina Bay on the central Oregon coast. The cost of living is very reasonable, especially compared to other west coast areas. Portland is about 2.5 hours north, and Corvallis is about 1 hour east.

Please email or call me with any questions, but be sure to apply according to the instructions in the official announcement below, including a cover letter that specifically addresses the required skills. The federal government can be very exacting when it comes to these details, and applications are filtered by human resources staff before being forwarded to scientists.

Sincerely, %%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
Mark D. Camara USDA/ARS Aquaculture Genetics OSU - Hatfield Marine Science Center 2030 SE Marine Science Dr. Newport, OR 97365

Office: 541-867-0296 Fax: 541-867-0138 Mailto: Mark.Camara@oregonstate.edu

**************** * OFFICIAL ANNOUNCEMENT: * ****************

USDA - Agricultural Research Service POSITION ANNOUNCEMENT

Announcement Type: ALL SOURCES/ALTERNATIVE MERIT PROMOTION Position Title: Biological Science Technician (Animal)

Series/Grade: GS-0404-06/07/08

Promotion Potential: GS-09

Salary: GS-06: $28,644 - $37,237 per annum

GS-07: $31,830 - $41,380 per annum

GS-08: $35,252 - $45,828 per annum

Type of Appointment: Permanent

Location of Position: Newport, Oregon

Announcement Number: ARS-X3W-3424

Opening Date: August 11, 2003

Closing Date: September 29, 2003

Area of Consideration: All U.S. Citizens

APPLICATIONS WILL ALSO BE ACCEPTED FROM USDA SURPLUS AND FEDERAL DISPLACED EMPLOYEES IN THE COMMUTING AREA.

DUTIES: The incumbent will be engaged in all aspects of a new research program in shellfish genetics and selective breeding using both quantitative and molecular genetics, including assisting with the spawning, rearing and evaluation of animals in the hatchery and field, but emphasizing molecular aspects, including but not limited to: marker development and high-throughput genotyping and gene expression analyses in the laboratory.

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at http://life.biology.mcmaster.ca/~brian/evoldir.html

OregonStateU SalmonGenetics

POSITION ANNOUNCEMENT

Oregon State University College of Agricultural Science Coastal Oregon Marine Experiment Station Faculty Research Assistant $25,000 - $35,000 (depending upon experience) Start date: 9/1/03

This 12-month, full-time, fixed-term appointment is with the Coastal Oregon Marine Experiment Station, located at Hatfield Marine Science Center in Newport, OR. Reappointment is at the discretion of principal investigator.

DUTIES: The duties and responsibilities of this position are: DNA extraction and microsatellite characterization of Oregons coastal chinook and coho stocks; new loci (microsatellite and other markers) characterization including inheritance tests; establishing contacts and collaborating with a coast-wide team including genetics labs in CA, WA, Canada and AK; population genetics analysis of results; report preparation for work performed and communicating these with the scientific community and assist with general research and learning in the Marine Fisheries Genetics program at Hatfield Marine Science Center.

QUALIFICATIONS: BSc in genetics, ecology or evolution with emphasis on statistics. Molecular genetics experience in PCR, DNA extraction. Demonstrated effective research in multi-user molecular genetics laboratory. Effective presentation with professional demeanor. Preferred qualifications include a demonstrable commitment to promoting and enhancing diversity.

TO APPLY: To apply, please provide a cover letter, curriculum vitae and contact details for at least three references by email to Michael.Banks@oregonstate.edu or by US Mail to OSU/Hatfield Marine Science Center, Attn: Michael Banks, 2030 SE Marine Science Dr., Newport, OR 97365. For full consideration, apply by August 18, 2003.

OSU is an Affirmative Action/Equal Opportunity Employer and has a policy of being responsive to needs of dual career couples.

Michael A. Banks Assistant Professor, Marine Fisheries Genetics Coastal Oregon Marine Experiment Station Hatfield Marine Science Center, Oregon State University 2030 SE Marine Science drive Phone: (541) 867 0420 Newport OR 97365-5229 Fax: (541) 867 0138 http://-www.marineresearch.oregonstate.edu/genetics/

PortlandOR FishEvol

Quantitative Fisheries Scientist Fish Science Department Columbia River Inter-Tribal Fish Commission Portland, Oregon

The Commission invites applicants for for a permanent full-time fisheries scientist working in ecology/evolutionary biology. We seek candidates with interests and backgrounds in ecology and evolution of fishes who will complement a team that includes specialists in molecular evolution, population dynamics, fishery science, aquaculture and ecology. We are especially interested in candidates investigating the risk and benefits of artificial progagation of endangered species in natural systems. The incumbent will work closely in research and monitoring of restoration projects implemented throughout the region.

The Department has strong research ties with the University of Idaho and its activities are partly based in the soon-to-be expanded Hagerman Fish Culture Experimental Station in Hagerman, Idaho. Collaborative

research with University scientists is strongly encouraged. The position is based at the head office in Portland, Oregon.

The successful candidate will be provided with a competitive start-up package and will be expected to establish a externally funded research program. Existing project funds are in place for at least 2 years. For more information, see our web site at http://-www.critfc.org . Candidates should send a curriculum vitae, a statement of interest, and representative publications, and three references to: Janelle Anderson, HR Coordinator, Columbia River Inter-Tribal Fish Commission, 729 NE Oregon, #200, Portland, OR 97232, andj@critfc.org, Fax: 503-235-4228. Additional Information: André Talbot, Senior Fisheries Scientist (503) 238-0667 tala@critfc.org

Closing Date: September 15, 2003

Andre Talbot <TALA@critfc.org>

QueensU ComputationalBiol

QUEEN'S UNIVERSITY - The Department of Biology invites applications for a Tier I Canada Research Chair in biological imaging and computational biology. Preference will be given to candidates with proven leadership in building a research group using dynamic imaging and quantitative, experimental methods to investigate topical areas such as the dynamics of protein localization, signal transduction or morphogenesis. The successful applicant will be selected primarily on the basis of overall excellence, but should complement existing research programs at Queen's which use imaging and biosensor technology to answer questions in cell biology, neurobiology or development. The Department of Biology has superb facilities in the new Biosciences Complex, and access to a state-of-the-art Protein Function Discovery proteomics facility (www.queens-pfd.ca). Queen's University is a medium-size university with a full range of professional programs including a medical school, providing opportunities for collaborations involving faculty from other academic units such as Biochemistry and the School of Computing. Queen's is recognized nationally for the quality of its undergraduate and graduate programs, which attract outstanding students. Kingston is an attractive community of approximately 150 000, situated on the shores of Lake Ontario, close to Ottawa, Montreal and Toronto. Qualifications for this position include a PhD, postdoctoral experience and published evidence of excellent research ability. The successful candidate will be expected to be an excellent teacher and to develop a vigorous, externally funded research program. Applicants must be eligible for nomination to a Canada Research Chair (CRC), Tier 1 that has been allocated to this position (www.chairs.gc.ca) and brings with it substantial infrastructure funding from CFI/OIT. A separate CFI/OIT proposal for major new instrumentation and infrastructure in this area at Queen's has also been submitted. Tier 1 CRCs are normally more than 10 years from PhD at the time of application and will be appointed at the level of Associate or Full Professor depending on qualifications. Expected date of appointment is July 1, 2004, subject to negotiation. Review of applications will begin November 12, 2003 and continue until the position is filled. Prospective candidates requiring additional information about this position may contact the Head of Biology in confidence prior to the deadline. Formal applications require submission of curriculum vitae, statement of current and prospective research interests, statement of teaching interests, and at least three letters of reference to: Dr. Peter T. Boag, Head, Department of Biology, Queen's University, Kingston, Ontario, Canada K7L 3N6 (Web: biology.queensu.ca, E-mail: biohead@biology.queensu.ca, Fax: (613) 533-6617). Academic staff at Queen's University are governed by a collective agreement, the details of which are posted at www.queensu.ca/qufa. In accordance with the Queen's guidelines for the assignment of Canada Research Chairs, applications from qualified women are particularly encouraged for this position. Queen's University is committed to employment equity and welcomes applications from all qualified men and women, including visible minorities, aboriginal people, persons with disabilities and persons of a diversity of sexual orientation. Canada Research Chairs are open to candidates of all nationalities. However, Canadian citizens and permanent residents will be considered first for this position. –

Dr. Peter T. Boag, FRSC Professor and Head of Biology Department of Biology Rm. 3102 Biosciences Complex Queen's University Kingston, Ontario Canada K7L 3N6

EMAIL: boagp@biology.queensu.ca PHONE: (613) 533-6132 FAX: (613) 533-6617 WEB: http://-biology.queensu.ca

Toronto Bioinformatics

Tm Bioscience Corporation

Tm Bioscience is a DNA-based diagnostics company developing a suite of genetic tests that can be applied to drug discovery and patient diagnosis. If you are looking for an aggressive growth, leading edge Canadian genomics company, consider Tm Bioscience.

Bioinformatics Specialist

The Bioinformatics and Computational Biology (BCB) Group of Tm Bioscience is currently seeking a highly capable and motivated individual to perform bioinformatics related tasks, as well as assist with software development and research projects associated with the genetic assays developed by Tm Bioscience. The BCB Group develops and applies computational tools and application programs for use by the company's research scientists, and develops software to enhance Tm Bioscience's Tag-It Mutation Detection Kits. The successful candidate will report to the BCB Group managers.

A graduate degree in the biological or computational sciences is required, with candidates having industrial bioinformatics experience being preferred. The successful candidate will have demonstrated cross-disciplinary skills in the biological and computer sciences, and will be able to interact with scientists to define, design, and implement solutions to bioinformatics related problems. Solid experience with Perl and C++ are required, as well as knowledge and experience with sequence analysis software and databases, primer design, and basic data analysis.

Please mail, fax or e-mail your CV and a cover letter by September 15, 2003 to:

Human Resources Tm Bioscience Corp. 439 University Ave Suite 1050 Toronto ON M5G 1Y8 Fax: 416-593-1870 E-Mail: hr@tmbioscience.com

Only those candidates selected for an interview will be contacted.

Dan Fieldhouse <dfieldhouse@tmbioscience.com>

UFlorida ResTech

A position as LAB MANAGER/RESEARCH TECHNICIAN is available in the lab of Dr. Charles Baer in the Department of Zoology at the University of Florida. The position will begin October 1, 2003, although start date is somewhat flexible. Job Description: The successful candidate will be responsible for the day-to-day operation of a modern Evolutionary Genetics lab in which the nematode Caenorhabditis elegans (and relatives) is the primary research organism. Duties include preparation of media, worm husbandry, development of experimental protocols and resources (both live-animal and molecular), managing high-volume genotyping and sequencing projects, data and stock management, general troubleshooting, and supervising and training undergraduate research assistants. Necessary qualifications: The successful candidate must have excellent organizational and time-management skills, at least two years of relevant experience (e.g., in an academic lab or private industry), and references testifying to the candidate's ability to contribute positively to group morale.

Desired qualifications: Working knowledge of basic molecular biology techniques and bioinformatics (e.g., sequence editing and alignment, BLAST, primer design). Computer programming skills are a big plus. 2. Familiarity with sterile microbiological methods. Previous experience in a microbiology or C. elegans lab is a big plus.

Salary: Commensurate with experience and qualifications.

Please direct inquiries, including a cover letter and a CV or resume (preferably as an Email attachment) including the names and contact information of three references, to:

Charles F. Baer Assistant Professor Department of Zoology University of Florida P. O. Box 118525 Gainesville, FL 32611-8525 USA Phone: 352-392-3550 FAX: 352-392-3704 Email: cbaer@zoo.ufl.edu Web: http://www.zoo.ufl.edu/Faculty/baer.html

UGeorgia ResTech

A full-time research technician position is available immediately at the University of Georgia to work on the evolutionary genetics of aging in Drosophila. The position is for a minimum of 2 years.

The ideal candidate will be a detail-oriented person

with good communication skills, the ability to work independently and as part of a team, and someone with previous biology research experience. The job is well suited for someone interested in gaining research experience before going to grad school, and will include opportunities for independent research. Recent projects in the lab include work on lifespan variation in natural populations, sex- differences in aging, and the role of networks in aging.

The working conditions, intellectual atmosphere, and facilities in Genetics at Georgia are excellent. Athens is a lovely and inexpensive place in which to live with all of the advantages and culture of a 200-year-old university town. See the Department of Genetics web site at http://www.genetics.uga.edu . Review of applicants will begin immediately and will continue until the position is filled. Interested persons should send (by e-mail) a resume/CV (with GPA), a statement of current interests and future plans, and the names and contact information of 2 references to: Daniel Promislow promislow@uga.edu

Daniel Promislow <promislow@uga.edu>

UMontreal GenomicsBioinformatics

Greetings,

I would like to bring the appended job announcement to your attention. Please direct your correspondence NOT by replying to this mail, but either to jobs@bch.umontreal.ca , or via snail mail (see appended announcement).

Yours,

B.F. Lang Universite de Montreal, biochimie

RESEARCH POSITION

Comparative and Evolutionary Genomics/Bioinformatics. Faculty Position, Canadian Institute for Advanced Research

The Department of Biochemistry at the Faculty of Medicine invites applicants for a faculty position at the Assistant Research Professor level in the areas of Comparative and Evolutionary Genomics, and Bioinformatics. This position implies a prestigious Scholar appointment in the Evolutionary Biology Program of the Canadian Institute for Advanced Research (CIAR). The successful candidate will have demonstrated excellence in the field of bio- informatics and/or genomics. Preference will be given to candidates with experience in evolutionary biology. He or she is expected to establish an innovative research program, and participate in teaching at both the undergraduate and graduate levels. Salary and startup funds will be commensurable with qualifications and experience, and successful candidates will be eligible for con- siderable infrastructural support through the Canada Foundation for Innovation.

Applicants should hold a PhD in a relevant discipline, have post- doctoral experience and an excellent publication record. All qualified candidates are encouraged to apply, while citizens and permanent residents of Canada will be given priority. Review of applications will begin on 15 August, 2003, and will continue until a suitable candidate is found. Applications should include a current CV, a summary of accomplishments, future directions in research and teaching, and three letters of reference, to be sent to:

Dr. B. Franz Lang Departement de Biochimie Universite de Montreal 2900, Blvd. Edouard Montpetit Montreal, QC, H3Y 1J4, Canada E-mail : jobs@bch.umontreal.ca

Franz Lang <Franz.Lang@Umontreal.ca>

UOregon EcolEvol

The following ad appeared in the August 22 issue of Science:

TWO POSITIONS IN ECOLOGY AND EVOLUTIONARY BIOLOGY. The University of Oregon Center for Ecology and Evolutionary Biology (CEEB) and the Department of Biology seek applications for two positions in the fields of ecology and evolutionary biology. One position is at the ASSISTANT PROFESSOR level, while the other position may be filled at any rank. We are interested in Ecologists using experimental approaches to address ecological processes at any scale, including the microbial. We are also interested in Evolutionary Biologists using mechanistic approaches to address the evolution of gene function and the molecular basis of phenotypic evolution. We will consider exceptional candidates in other areas of ecology and evolutionary biology. The successful candidate will have an outstanding research program and a commitment to excellence in teaching. Ph.D. is required. Applicants should submit curriculum vitae, statements of research interests and teaching philos-

ophy, and three letters of recommendation to: Ecology/Evolution Search Committee, Department of Biology, University of Oregon, Eugene, OR 97403-1210. Website: http://evolution.uoregon.edu/. To assure full consideration, applications must be received by October 15, 2003. The University of Oregon is an Equal Opportunity/Affirmative Action Institution committed to cultural diversity and compliance with the Americans with Disabilities Act.

Patrick C. Phillips, Associate Professor of Biology Center for Ecology and Evolutionary Biology Email: pphil@uoregon.edu Phone: (541) 346-0916 | FAX (541) 346-2364 Address: 5289 University of Oregon Eugene, OR 97403-5289 USA Web: Lab http://www.uoregon.edu/ ˜ pphil EvoNet http://-www.EvoNet.org CEEB http://evolution.uoregon.edu IGERT http://evodevo.uoregon.edu

UPuertoRicoRP 3 MolSyst

I wanted to call people's attention to three positions currently open at the University of Puerto Rico-Rio Piedras (UPR-RP). Two, the Genetics and Molecular Systematics positions, are particularly appropriate for the readership of Evoldir. UPR-RP is well equipped for molecular research and there are ample scientific opportunities for individuals interested in the ecology and evolution of tropical organisms. Of course, the climate is also nice. We have an active core of researchers and are seeking to build on our strength in ecology and evolution. We will continue to collect applications until the the first or second week in September and I encourage interested researchers to apply.

Owen McMillan wmcmilla@rrpac.upr.clu.edu http://-zephyr.hpcf.upr.edu/ ˜ mcmi-lab/ ********** FACULTY POSITIONS AT THE UNIV. OF PUERTO RICO Genetics/Molecular Systematics/Proteomics-Structural Biology The Department of Biology of the University of Puerto Rico at Rio Piedras invites applications for 3 tenure-track positions in: (1) Genetics-Molecular to Population, (2) Molecular Systematics-Animal or Plant and (3) Proteomics or Structural Biology. The candidate is expected to develop an active research program and to teach at the graduate and undergraduate levels. Candidates must hold a Ph.D. or equivalent and have postdoctoral experience. Interested candidates should send résumé, a statement of current and future research and teaching goals, representative publications and 3 letters of reference to: Dr. Alberto Sabat, Box 23360, UPR Station, San Juan, PR 00931-3360 or email: asabat@upracd.upr.clu.edu. Applications will be reviewed from June 16, 2003, until the positions are filled. Expected start date is August 2004. University of Puerto Rico is an Equal Opportunity Employer. –

W. Owen McMillan Associate Professor Department of Biology University of Puerto Rico- Rio Piedras P.O. Box 23360 San Juan, PR 00931-3360

wmcmilla@rrpac.upr.clu.edu phone (office): 787-764-0000 [(1)2909] phone (lab): 787-764-0000 [(1)2902, (1)2853] phone (home): 787-764-3564 fax: 787-764-3875

Owen McMillan <wmcmilla@rrpac.upr.clu.edu>

Vienna GeneticsLabTech 2

Genetics Laboratory Technician Position Konrad Lorenz Institute of Comparative Ethology, Vienna, Austria

We are searching for a highly organized, reliable and motivated genetics laboratory technician. We are particularly interested in applicants having experience with vertebrate genomes, especially house mice, birds, or fish, and conducting paternity analyses. Competitive applicants will have excellent bench skills using molecular genetic techniques (such as DNA extractions, microsatellite typing, PCR, DNA fingerprinting, fluorescent gel analysis, Southern blots, etc.), basic computer skills, and must be capable of working independently. German would be useful, but it is not necessary as KLIVV is an international institute that communicates in English. Salary depends upon experience and skills. Review of applications begins immediately and will continue until the position is filled. The starting date is flexible.

The Konrad Lorenz Institute is located in the Vienna Woods, on the outskirts of Vienna (see http:/-/www.oeaw.ac.at/klivv/). Vienna has several laboratories that use molecular genetic techniques, including the Research Institute of Wildlife Ecology, University of Veterinary Medicine, which is located next door. Vienna offers excellent public transportation, excellent schools, cultural activities, and outdoor recreation opportunities (http://www.oeaw.ac.at/klivv/).

To apply send a CV, an application letter, and two letters of reference by e-mail (or regular mail, see address below) to Dr. Angela Pauliny (A.Pauliny@ klivv.oeaw.ac.at) .

Dr. Angela Pauliny, Genetics Technician Konrad Lorenz Institute of Comparative Ethology Austrian Academy of Sciences Savoyenstrasse 1a A-1160 Vienna, Austria Tel: +43 1 486 21 21 38 Fax: +43 1 486 21 21 28

Angela Pauliny <A.Pauliny@klivv.oeaw.ac.at>

Other

AMOVA intraindividual

Hi there!

I'm coming across some trouble with the analysis of my data and would appreciate some ideas on how to proceed:

We are working with ITS sequences for phylogeographic studies and for some individuals (20%) we have found intraindividual variation. After clonning them, the amount of variants found within each of these individuals has been pretty different, ranging from 2 to 7. So for all the individuals analyzed the majority have only one allele, but within these 20%—> 2,3,4 or 7 different alleles have been found.

In order to compare how the extent of intraindividual variation relates to interindividual variation we have think of an AMOVA. Arlequin seems the good programe to use but my doubt is that although this program seems to work with genotypic data, I'm afraid that for genotypic data they assume biallelic data....and for this mulpicopy marker that shows a higher number of alleles per individual I don't know how to organize the file.

has anybody dealt with this problem before?

I will appreciate any idea!

Thanks a lot!

Sandra Duran

PhD student Facultat de Biologia. Dept. Biologia Animal, Invertebrats. Av. Diagonal, 645. 08028 Barcelona CATALUNYA

Phone: +0034 934021441 Fax: +0034 934035740 e-mail: sandra@porthos.bio.ub.es e-mail: sandra@porthos.bio.ub.es

AMOVA intraindividual answers

Dear all,

First of all I would like to thank all the people that have given me ideas and opinions about interindividual vs. intraindividual AMOVA with multi-copy markers as ITS. As many people asked me to send them the answers, I've decided to post them in the list.

To summarize, although the best option could be to treat each individual as a population, that is, treating each allele within an individual as an haplotype within a population, even if we could know how many copies of the ITS are present in the genome of the organism studied, it would probably be very difficult to know how many copies are present for each of the different variants. Thus, as the frequency of each distinct allele within each individual is unknown, it is kind of tricky to compare inter and intraindividual variation with multi-copy markers with the AMOVA.

——— HERE IS THE QUESTION I SENT—-> The organism of study is a sponge ——— > We are working with ITS sequences for phylogeographic studies and for > some > individuals (20%) we have found intraindividual variation. After > clonning > them, the amount of variants found within each of these individuals > has been > pretty different, ranging from 2 to 7. So for all the individuals > analyzed > the majority have only one allele, but within these 20%—> 2,3,4 or 7 > different alleles have been found. > > In order to compare how the extent of intraindividual variation > relates to > interindividual variation we have think of an AMOVA. > Arlequin seems the good programe to use but my doubt is that although > this > program seems to work with genotypic data, I'm afraid that for > genotypic > data they assume biallelic data....and for this mulpicopy marker that > shows > a higher number of alleles per individual I don't know how to organize > the > file.

HERE ARE THE ANSWERS

You may want to back up a bit an do the AMOVA with the original AMOVA 1.5 program. In addition to not having a cryptic file format, it works on the distance matrix directly. You would have to come up with an appropriate distance metric (see Excoffier & Smouse paper on Molecular Variance Parsimony for a method appropriate to sequence stuff). In fact, you could just do it 'by hand' if your so inclined once you define the distance metric.

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from your message it is a bit difficult to give advise because you did not tell wich which species you are working. Are they diploid? Could some of them be hybrids (including ancient hybrids)? Did you check for PCR chimaeras? (The problem was described in detail by Cronn, R., Cedroni, M., Haselkorn, T., Grover, C., Wendel, J.F. (2002) PCR-mediated recombination in amplification products derived from polyploid cotton. Theor. Appl. Genet. 104: 482-489, not for ITS, but with ITS the problem might be worse because of the high copy numbers.) What is the approximate evolutionary age of your species? Concerted evolution might not yet have homogenized the ITS copies. Also, there are papers that e.g. in hybrids can occur asymmetric elimination of specific ITS types and so on. The same might happen at intraindividual level to make it unpredictable how many variants survive of will be found in your samples. Can you exclude contaminations? So, the whole field is rather complex. Maybe it helps to browse the literature (not necessarily the phylogeography literature only) for the tricks and pitfalls of the ITS. Maybe that can give you an idea what might be possibly going on with your data set.

Two immediate reactions are that individuals with 'clean' sequence traces would probably show intraindividual variation if you cloned (this was our experience) and that AMOVA should work if you treat each individual as a haploid population (eg by pretending that the sequences are mitochondrial).

While I have not dealt specifically with the analysis of data such as yours, I have had some experience with ITS paralogy in plants, where it has been well documented. I do not know what methodology you are using to clone the ITS paralogs, but if it involves PCR from genomic DNA, I would urge you to use caution in proceeding with your analysis. This is because the number of alleles you isolate from any individual may not represent the actual number in the genome. My experience (in plants only) suggests that you might get just one allele from one amplification, but get several alleles from a second amplification of the same template. The paper cited below (which you may already be aware of) suggests some possible reasons for this, in light of the competitive nature of PCR. If stochastic amplification of paralogs is occuring in your samples, I think that the results of the AMOVA you

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at http://life.biology.-mcmaster.ca/~brian/evoldir.html

Allozymes angiosperms

Hello-

Does anyone have experience doing allozyme work on cellulose acetate in angiosperms? I'm using a lithium-borate buffer solution that gives good, dark bands, but every individual I screen appears monomorphic. I've even started genotyping various species I know to be highly variable, and no heterozygotes. The bands aren't very fine, so I'm beginning to wonder if the grinding and running buffers I'm using just aren't giving me the resolution I need. If you have any suggestions I'd really appreciate it.

Sincerely, Robin Smith (ras10@duke.edu)

Robin Smith Graduate Student Duke University Department of Biology Box 90338 Durham, North Carolina 27708

Brachypodium samples

Hello,

Are there any scientists willing to send me some Brachypodium sylvaticum seed from native ranges (Europe, Middle East, Asia)? I'm starting my PhD project on the evolution of invasive species. B. sylvaticum is a new invasive in Oregon, and I want to compare native populations to the ones here. I'm especially interested in populations from India, as we have some information indicating that some of the first introductions in Oregon may have originated from the Nilgiri Hills of Utakamand, in Madras. Also Turkey, Greece, Iran, Spain, Yugoslavia, Australia, or Kazakhstan. If you can help, please let me know. I'd love to collect the seed myself, but I don't have the funds at the moment for all that travel.

Thanks, Alisa Ramakrishnan Portland State University aramakris@yahoo.com

Collaboration hostparasites

Plea for Collaboration-

Hello, my name is Jessica Light and I am a Ph.D student at Louisiana State University working on a molecular analysis of host-parasite cophylogeny. My research concentrates on the sucking lice of rodents, with a focus on heteromyids and their lice. While I have collected lice from a majority of the North American heteromyids, I am looking to form collaborations to collect Central and South American heteromyids and their lice.

The collaboration I propose will actually save you time in the field. You simply measure, weigh, tissue, and skin the animal, then freeze the skin in a foil pouch in liquid nitrogen or dry ice. After I examine the skins for ectoparasites, I will prepare the specimen for you as a study skin or skeleton, whichever you prefer. Also, I will wash the skin, so any blood and dirt will be removed. This method has worked for well for hundreds of specimens I have collected.

I have a detailed protocol explaining how my method works and can pass that on to anyone who might be interested.

While my interests do lie with the heteromyids, I will gladly examine other rodent specimens for lice and other ectoparasites.

Please contact me at jlight2@lsu.edu if you are interested.

– Jessica E. Light Museum of Natural Science Louisiana State University 119 Foster Hall Baton Rouge, LA 70803-3216 225-578-5393 (office) 225-578-3075 (fax) http://www.museum.lsu.edu/~light/light.html http://-/www.museum.lsu.edu/~light/light.html

DNAladder accuracy

For pcring microsatellite loci from genomic dna, I need to quantify dna before putting 100 ng dna in a 25 uL PCR RX. As spectrophotometers and flourometers can give inaccurate ng/uL readings, I consider using Invitrogen's low dna mass ladder: is the ladder accurate?

AEM Baker mouse@lamar.colostate.edu

Daphnia Evolution

DAPHNIA EVOLUTIONARY GENETICS AND GENOMICS

We wish to call attention to two significant developments in the field of Daphnia genetics and genomics that we hope will be of interest to students, postdocs, and other established scientists.

In brief, with more details given below:

1) The Joint Genome Institute will be sequencing the entire nuclear genome of Daphnia pulex within the next few months. This information, along with numerous other genomic tools under development, should rapidly transform D. pulex into a premier system for a wide array of studies in ecological and evolutionary genomics.

2) A multidisciplinary group of investigators has recently been awarded a substantial grant from the NSF FIBR program to use Daphnia to study The Causes and Consequences of Recombination.

3) The Second Annual Daphnia Genomics Consortium (DGC) meeting will be held in Manchester, NH on 8-9 September.

Daphnia Genomic Resources

In addition to the soon-to-be-complete genome sequence of D. pulex, a broad spectrum of other genomic tools are being developed by DGC members, most of which should be fully available within the next 12 months. These include: 1) arrayed, fingerprinted, and end-sequenced 10-fold redundant BAC libraries for both D. pulex and D. magna; 2) an arrayed 8-fold redundant cosmid library; 3) high-density genetic map based on ~1000 microsatellite markers; 4) collection of ~50,000 sequenced cDNAs; and 5) microarrays based on these cDNAs. DGC members are also currently developing methods for genetic transformation, cell culture, and RNAi. This rich genomic tool box, along with the unusual life-history features of Daphnia (the ability to clone, outcross, or self) and the ability to resurrect ancient genotypes (up to 1000-year old) by hatching eggs from lake sediments, should rapidly transform D. pulex into one of the most powerful systems for both laboratory and field-based studies in genetics and genomics. The DGC is an international group of supportive scientists, with a policy of open sharing of resources, anxious to recruit new investigators to the system. For some further information, see:

<http://daphnia.cgb.indiana.edu/>http://-daphnia.cgb.indiana.edu/ .

NSF FIBR Grant on the Causes and Consequences of Recombination

This recent research grant provides a number of opportunities for graduate-student and postdoctoral research in the following laboratories, over the next five years. Interested students and postdoctoral candidates are encouraged to contact any of the coPIs listed below. An overview of the planned research is given below.

Justen Andrews, Center for Genomics and Bioinformatics, Indiana Univ. functional genomics Jeffrey Boore, DOE Joint Genome Institute genome sequence development Carla Cáceres, Animal Biology, Univ. Illinois population biology and limnology John Colbourne, Center for Genomics and Bioinformatics, Indiana Univ. genomics Elizabeth Housworth, Mathematics / Biology, Indiana Univ. mathematical modeling Tom Little, Population Biology, Univ. Edinburgh parasites and sex Curt Lively, Evolution, Ecology, and Behavior, Indiana Univ. parasites and sex Michael Lynch, Biology, Indiana Univ. quantitative genetics and genome evolution Barrie Robison, Biology, Univ. Idaho genetic mapping W. Kelley Thomas, Hubbard Center for Genome Studies, Univ. New Hampshire genomics Mimi Zolan, Molecular Biology, Indiana Univ. meiosis

This project draws together an interdisciplinary team of researchers, further embedded in a broader consortium, with a unified goal of understanding one of biology's deepest mysteries –the evolutionary causes and consequences of recombination. The investigative team consists of cell biologists, ecologists, parasitologists, quantitative geneticists, genomicists, and mathematicians, all with considerable experience with specific aspects of recombination. The study organism, the planktonic microcrustacean Daphnia pulex, provides an exceptional array of opportunities for research in this area that is unavailable with any other system: a wide range of recombination intensities among natural populations, the presence of multiple sexual and asexual lineages, a powerful set of genomic tools, well understood ecology, ease of experimental manipulation, and a living-fossil record.

Project goals include: 1) development of high resolution genetic and physical maps to provide a key resource for the remainder of the project; 2) molecular and cytological characterization of the mechanisms underlying the transition from meiotic to mitotic progeny production; 3) evaluation of whether the mutation rate (including

the activity of mobile-genetic elements) is affected by an absence of meiosis; 4) study of the fates of nonsegregating alleles locked into asexual lineages, and a test of the

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at http://life.biology.mcmaster.ca/~brian/evoldir.html

Drawing networks answers

Hi there,

I recently (11th July) posted a question on the EvolDir relating to the use of the program Network 3.0. I was trying to determine a way of manipulating the network obtained when using the software.

Thanks to everyone who replied to this the ideas/solutions were very much appreciated. I also received a number of e-mails from people indicating that they were having similar problems, so I hope that the responses here may help. I have included a number of the suggestions I received. Several people had similar type ideas so I have tried to omit those that were similar in nature.

Generally there were three main approaches to solving the problem.

1. Use some sort of graphics converter to convert the bmp file to a file that can be manipulated (A few ways of doing this see below).

2. Brute force if the network is relatively simple you can cut and paste into something like CorelDraw and then, using the various drawing tools, copy the image by drawing over it and then deleting the original bmp image. I did try this and for a simple network you can very quickly recreate it. You can then manipulate the colour, size etc. For a simple network this is probably the way to go.

3. Other people suggested using other programs such as TCS or MINSPNET. I have used TCS and the network obtained from that is easily manipulated in CorelDraw etc.

For those that asked, the program I was using was Network 3.1.1.1 and it can be downloaded by going to www.fluxus-engineering.com Thanks again to everyone who replied to the original question. As I have said I received a large number of replies and I have tried to include the major ideas in terms of solutions in the reponses I have included below. All the reponses however, were greatly appreciated good luck!

Andy Given

THE QUESTION (posted July 11, 2003)

We are currently using Network 3.0 to construct median joining networks from mitochondrial data. We are trying to work out a way to manipulate the outputted network (i.e. show the various populations represented for a single haplotype by using different colours for that circle in the network). It appears that the network can only be saved as a bmp file although it looks like emf may be an option in the future.

Does anyone have any bright ideas that would allow further manipulation of these images? What we would like to do is export the image to something like CoralDraw and be able to do further editing there.

Thanks for your help.

Andy Given

THE RESPONSES:

1. I just paste / import the bmp into CorelDraw to use as a guide for the final network that I then draw on a layer above, since as far as I know there is currently no other way to get a publication-quality figure. Obviously this can be time-consuming, so an emf or postscript output would be ideal. However, there doesn't appear to be much current development progress - many options appear to have been 'under development' for some time.

2. No doubt a thousand people will tell you about Graphic Converter, a shareware mac product that can be tried free and which is omni-capable fo file interchanges and totally reliable. Available from many sites i think. I have tried Version 4.b

3. I just saw you posting on EvolDir. I have used the Network program quite a few times and I have always ended up redrawing the network by hand. I think there really is no choice if you want to add say, pie charts in place of the nodes in order to display the population distribution of your haplotypes (corrected for differing population sample sizes...). I have a slightly acrimonious relationship with Corel draw (!) and I find the best way to do this is in Excel. Here you can easily do any data manipulations and create all your pie diagrams. The drawing tools are OK and you can use the grid as a background to layout your network. I just size the pie diagrams according to the grid based on appropriate frequency bins. You can draw it big and then copy and past it into Powerpoint to shrink it an appropriate size for publication. It is really a pain but unless

the network is really huge and complicated then I find this to be the simplest option. That's my suggestion - if you hear of a better way please let me know!

4. The way I work with the output from a variety of software is to create a pdf file. The problem with this method is that you need to be using Adobe Acrobat and Illustrator. When you Acrobat installed, you can always set your printer to Adobe Distiller instead of your actual line printer. When you set Distiller as the printer, your program will ask you for a file name and all output is saved as a pdf file. You have to be careful that the output would go to a single page. What this does is creates a vector graphic that you can then import into Adobe Illustrator and do all the manipulations that you want. I have learned to write files in Adobe

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This message has been arbitrarily truncated at 5000 characters. To read the entire message look it up at http://life.biology.mcmaster.ca/~brian/evoldir.html

Galerucella samples

Dear evoldir members

we are working on a project investigating speciation in the Galerucella complex. These are beetles from the Chrysomelid family occurring on a range of host plants. Our focus is on Galerucella nymphaeae, the waterlily leaf beetle, which feeds on waterlilies (Nymphaeae alba, Nuphar lutea) and on Polygonaceae species (Rumex hydrolapathum, Polygonum amphibium) as well as a number of other species. For a large phylogeographic study we are searching for samples to complement our own range of samples. We are looking for samples from all over Europe, but are also interested in samples from North-America and Asia. For reference we would also be very grateful for samples from related species (G. pussila, G. calmariensis occurring on purple loose strife; and any other G. species). We would be very happy with any help here. It is not much work, once you are in a pond or river sampling the beetles is just 15-30 minutes work. For any details on how to sample and how to preserve the beetles please contact

Joop Ouborg (joopo@sci.kun.nl)

or

Arjan Borghuis (Arjan.borghuis@sci.kun.nl)

For any background on this project see:

Pappers, S.M., van der Velde, G., Ouborg, N.J., van Groenendael, J. M. (2002) Genetically based polymorphisms in morphology and life history associated with putative host races of the water lily leaf beetle Galerucella nymphaeae. Evolution 56:1610-1621

Pappers, S. M., Van der Velde, G., and Ouborg, N. J. (2002). Host preference and larval performance suggest host race formation in Galerucella nymphaeae. Oecologia, 130, 433-440.

Pappers S.M., van Dommelen H., van der Velde G. & Ouborg N.J. 2001. Differences in morphology and reproductive traits of Galerucella nymphaeae from four host plant species. Entomologia Experimentalis et Applicata 99: 183-191

or visit our website: http://www-eco.sci.kun.nl/-popbiol/welcom1EN.htm Your help will be highly appreciated!!!!!

Joop Ouborg Arjan Borghuis

Joop Ouborg <joopo@sci.kun.nl>

Genetic architecture

Please could you post the following:

Is anyone aware of programs that evaluate the genetic arhitecture of traits (ie. one that implements joint scaling tests or other related analyses)? Many thanks in anticipation.

Peter.

Peter Hargreaves <peterjhargreaves@hotmail.com>

Indel vs substitution

Can anyone out there help me with a citation that answers the following:

Do homologous protein coding gene sequences tend to diverge faster in sequence identity (i.e. nucleotide substitutions) than they do in length?

My suspicion is 'yes', but ideally I'd like to find a *very* general quantitative corroboration of this (i.e. pooled

across many protein families, across major phyletic lineages) - a short, robust answer one way or the other.

I feel that it's so obvious a question that someone must have asked it, probably very early on (sorry if it's something I really ought to know!), but maybe it's so obvious or so daft a question that noone has?

Thanks in advance for your collective grey matter, Steve Freeland

freeland <freeland@umbc.edu>

MicroMutRateArabidopsis

I've been doing a literature search of microsatellite mutation rates and have not been able to find microsat mutation rates for Arabidopsis. If somebody knows where I might be able to find this information, please e-mail me the citation(s) at tmarria@ku.edu.

Sincerely, Tara Marriage

Tara N. Marriage Ph.D. Student Department of Ecology and Evolutionary Biology University of Kansas 1200 Sunnyside Ave. Lawrence, KS 66045

Lab phone: 785-864-3763 E-mail: tmarria@ku.edu

tmarria <tmarria@mail.ukans.edu>

Phylogeography question

I am working on the phylogeography of a common butterfly (Hesperia comma), and I have a question about using programs like ARLEQUIN (or GEODIS or TCS) to analyze nuclear sequences that are polymorphic at a number of locations. Should I take every sequence and break it into two forms (for the different alleles), or can I enter the sequences with the polymorphic codes (Y, R, etc)? It seems like the former would be a nice option, because I could then make a minimum spanning network to visualize the alleles–but is that a kind of pseudo-replication to get two sequences out of one individual? People clearly use these programs with nuclear data in publications, but I have not been able to find one where the methods are stated explicitly. Thanks.

Matthew L Forister Section of Evolution and Ecology 2320 Storer Hall University of California One Shields Ave. Davis, CA 95616

lab phone:(530) 752-2225 home phone:(530) 297-0797 mlforister@ucdavis.edu

Phylogeography question answers

A number of people asked that I provide a summary of the replies from my question. Briefly, this is what I asked: what should I do to generate haplotypes from nuclear sequences with a number of polymorphic sites (so that I can use programs like TCS and ARELQUIN)?

It seems that it's a pretty messy business trying to infer such haplotypes (without actually doing more lab work). However, one program was recommended by a number of people, and that's PHASE. A reference for that is:

Stephens, M., N.J. Smith, and P. Donnelly, A New Statistical Method for Haplotype Reconstruction from Population Data. Am. J. Hum. Genet., 2001. 68: p. 978-989.

An alternative method might be found in: Clark, A. G. 1990. Inference of haplotypes from PCR-amplified samples of diploid populations. Mol. Biol. Evol. 7: 111-122.

Hope that is of use to someone. Thanks! –Matt

= = = = = = = Matthew L Forister Section of Evolution and Ecology 2320 Storer Hall University of California One Shields Ave. Davis, CA 95616 = = = = = lab phone:(530) 752-2225 home phone:(530) 297-0797 = = = = = = = = mlforister@ucdavis.edu

PlantGrowthRoom equipment

I am a plant developmental biologist retreaded to an ecological economist and environmental science educator. The walk in growth rooms I had constructed in the mid 1980s are being dismantled and put in the trash. One has gone and three more are to go in the near future (probably in Sept 2003).

For the cost of packing up and transport, another institution could have our sodium vapor – metal halide

lamp fixtures with ballasts, air handlers, air filters, and other small stuff. The lights give good spectral quality of about 50% sunlight. The Boyce Thompson Inst at Cornell had the prototype we copied.

Contact me if you have interest.

Carl McDaniel Dept of Biology Rensselaer Polytechnic Institute 110 Eighth Street Troy, NY 12180

mcdanc@rpi.edu (518) 271 6563

Reliable PowerSupply

The most we can spend is $1 000 for a 2000 volt electrophoresis power supply. Does anyone have experience with reliable power supply in this price range? AEM Baker mouse@lamar.colostate.edu

Software GEDA GEDS

The University of Pittsburgh offers online versions of the Gene Expression Data Analysis tool (http://bioinformatics.upmc.edu/GE2/GEDA.html) and the Gene Expression Data Simulator (http://-bioinformatics.upmc.edu/GE2/index.html).

Options for Analysis in the GEDA web application include:

Transformation Log2,Log10,Ln

Normalization Multiplicative Biases Within-Array Sum, Median, Mean, Quantile, Trimmed Mean Among-Array Minimum Mean and Median Mean Ratios Additive Biases Global Mean Adjustment (new) Max1,Min0 Z-transformation Nonlinear Normalization (to be added soon) Computation of averages of duplicate genes

Tests for Differentially Expressed Genes include J5 test (new) Simple t Pooled Variance t SAM test (Tusher et al., 2001) Simple Separability (new) Weighted Separability (new) 3 types of 'fold-change' S:N BSS/WSS All of the above as parametric threshold tests or as permutation tests All of the above with mean, median or trimmed mean

Special Options Jackknife step to reduce false positives MDSS Algorithm (Lyons-Weiler et al., 2003)

Unsupervised and Supervised Sample Clustering 6 Distances for Clustering 5 Clustering algorithms (1 new)

Unsupervised and Semi-supervised Gene Clustering (to be added soon)

Computational Validation Leave-one-out validation Cross-fold validation Cross-fold validation with a variable threshold Nonparametric boostrap

The output includes:

Plots Frequency Distribution MeanA vs. MeanB Mean vs. Variance M-A plot Clustering Results (Diagram or Tabular) Distance Matrix Test score histogram (colored and sorted) Mean value histrogram (colored and sorted) Score Frequency Distribution

Table of links for of differentially expressed genes in -LocusLink -GenomeView -UCSC -ensemble -UniGene -dbSNP -AmiGO -OMIM

The GEDA tool has refined annotation (http://bioinformatics.upmc.edu/Help/-GEDADescription.html)

and support in the form of a news group http:/-/groups.yahoo.com/group/GEDANews We provide constantly updated recommendations for analysis http://bioinformatics.upmc.edu/Help/-Recommendations.html based on results from the simulator.

Users can upload data from their drive. We also offer 8 published cancer data sets 'on tap'as well as links to other published data sets http://-bioinformatics.upmc.edu/Help/UPITTGED.html and a constantly updated "Related Literature" http://bioinformatics.upmc.edu/Help/-MicroarrayReferences.html The web applications are constantly upgraded and free for academic use. We have collaborators at seven institutions, in the US & Canada; mirrors should be available later this year.

Lit Lyons-Weiler J, Patel S, Bhattacharya S. (2003) A classification-based machine learning approach for the analysis of genome-wide expression data. Genome Res Mar;13(3):503-12.

Tusher VG, Tibshirani R, Chu G. 2001. Significance analysis of microarrays applied to the ionizing radiation response. Proc Natl Acad Sci USA 98,5116-21.

~ Jim

James Lyons-Weiler Assistant Professor Department of Pathology/ Center for Pathology Informatics/ Center for Oncology Informatics/ University of Pittsburgh Cancer Institute/ http://bioinformatics.upmc.edu/ Address: UPMC Cancer Pavilion 5150 Centre Ave

Pittsburgh, PA 15232

Phone: (412) 623-7866 Cell: (412) 537-5390 Fax: (412) 647-5380 Email:lyonsweilerj@msx.upmc.edu

"Lyons-Weiler, James" <lyonsweilerj@upmc.edu>

Software TRACER v1 0

Tracer v1.0

This is a graphical program for analysing the output of Bayesian MCMC software including our program BEAST and the popular MrBayes.

BEAST - <http://evolve.zoo.ox.ac.uk/beast/> MrBayes - <http://morphbank.ebc.uu.se/mrbayes/> It can plot the traces, estimate autocorrelation, plot posterior densities and give confidence intervals. It can also compare and combine output from multiple runs. It can be used to look for convergence, select burn-ins and check for adequate chain length. For each parameter it can estimate the Effective Sample Size (ESS) - the number of effectively independent draws from the posterior distribution that the Markov chain is equivalent to.

It can produce publication quality output either as SVG graphics or by Printing to PDF if available (i.e., Mac OS X).

Note that this program analyses the continuous parameters of the models (i.e., not the trees) - for MrBayes this means the '.p' files and for BEAST the '.log' files.

Versions of this software are available for Mac OS X, Linux, Unix and Windows:

<http://evolve.zoo.ox.ac.uk/software/tracer/>

Andrew Rambaut & Alexei Drummond

–

Andrew Rambaut, EMAIL - andrew.rambaut@zoo.ox.ac.uk Zoology Department, WWW - http://evolve.zoo.ox.ac.uk/ University of Oxford, TEL - +44 1865 271261 South Parks Road, Oxford, UK FAX - +44 1865 271249

TagIT software

TagIT software for tagging SNP selection and analysis

The latest version of this software (ver 1.17) is available for download (free for non-commercial use) from http://popgen.biol.ucl.ac.uk/software.html

TagIT is a set of functions to facilitate analysis of linked SNP genotypic data in order to identify a small set of 'tagging' SNPs (also known as 'haplotype tagging' SNPs) which can be used in future association studies to look for unknown causal SNPs within the region.

Briefly, TagIT functions perform the following:

1) Input and cropping of linked genotypic data - either of unrelated individuals or of trios (mother+father+child).

2) Check for Mendelian inconsistencies in trios (i.e. incompatible child's genotype given parents' genotypes).

3) Tests for HW equilibrium at each locus.

4) In trio data, return all completely resolved haplotypes (i.e. complete parental haplotypes with resolved phase).

5) Combine resolved haplotypes with unresolved data in an EM algorithm to estimate haplotype frequencies in trio data (algorithm also works on unrelated data is necessary). To our knowledge, this is the only such EM algorithm available for trio data.

6) Calculate pairwise LD measures and P-values using haplotype frequency data.

7) Display LD measures using grid plots.

8) Provide "best" tSNP sets of various sizes, according to one of a number of different criteria, including r-squared based criteria appropriate for association studies.

9) Assess the ability of "best" tSNP sets to associate with loci that have been dropped from the set used to derive the tSNP, to help assess an optimal tSNP set size designed to look for an unknown causal SNP in a future association study.

A comprehensive user guide is available. The TagIT software can be seen "in action" in the following forthcoming publications:

Weale ME et al. (2003) "Selection and evaluation of 'tagging' SNPs in the neuronal sodium channel gene SCN1A: Implications for linkage disequilibrium gene mapping" Am J Hum Genet (in press)

Goldstein DB et al (2003) "Genome scans and candidate gene approaches in the study of common diseases and variable drug responses", Trends in Genetics (in press)

TagIT functions work within the MATLAB environment (http://www.mathworks.com/) or within the free GNU version of MATLAB, Octave (http://-www.octave.org/).

To cite TagIT please use: TagIT. Version 1.17. 2003. Michael E Weale and David B Goldstein.

Sincerely,

Mike Weale The Centre for Genetic Anthropology Department of Biology University College London Darwin Bdg, Gower St, London WC1E 6BT m.weale@ucl.ac.uk

equipment questions

I have two equipment questions.

1) We (Walt Eanes' Lab) are looking to scale up to using a UV/visible wavelength microplate reader for Vmax and various metabolite concentration measurements. Does anyone have suggestions as to a good (or bad for that matter) spec. that we should look into?

2) I'm looking to purchase a cellulose acetate electrophoresis rig on which to run allozymes for a teaching lab. I'm having a hard time locating the old Gelman (now Pall) rig that I have used in the past. Does anyone know of a good, currently available, set up?

Thanks in advance for any help that can be offered.

Thomas Merritt Dept of ecology and Evolution SUNY-Stony Brook

thomas merritt <merritt@life.bio.sunysb.edu>

mtDNA extraction species status

Dear EvolDir members Good to be back reading EvolDir messages again I have been out of the system for a while.I hope someone will be happy to advise me on some of the following queries. I have not undertaken mitochondrial work (my area was microsats) but have been asked to look into this area to advise a group who are wanting to set up a project in this field. The group wish to use molecular data to examine 3 sub-species of parrot and hope to provide evidence for single species status for one of these birds along with other morphological/distributional data they have collected.I would be grateful if anyone would provide comments or advise on any or the following queries that I have.I seem to remember that there can be some problems isolating mitochondrial from nuclear DNA during the extraction process. And that this may often be a problem with birds Are special extraction protocols required/recommended?With regard to species / sub-species discrimination:What length of bp is it recommended overall to sequence to enable species discrimination?Which are the most appropriate regions cytochrome b? is this best combined with another region/regions?Can anyone recommend primers that might be useful in parrots.Is there a recognised distance or percentage divergence that is accepted as appropriate for separating sub-species into species? Or what are the most appropriate techniques for this analysis?What number of individual birds are required to confirm consensus between individuals within each species/sub-species.Thanks for your help all comments and advice will be gratefully received.Tee Taylor

Tiawanna Taylor <201512493@nu.ac.za>

mtDNA extraction species status answers

Hi all

Thanks for the great response to my request for help it was really appreciated. I have delayed in sending in the answers as a virus hit my local network. I know that my system had some problems and I hope that I received all your replies. Below is a copy of my original message followed by the main points from replies I received.

Thanks again everyone. Tiawanna

THE QUESTION Dear EvolDir members Good to be back reading EvolDir messages again I have been out of the system for a while.I hope someone will be happy to advise me on some of the following queries. I have not undertaken mitochondrial work (my area was microsats) but have been asked to look into this area to advise a group who are wanting to set up a project in this field. The group wish to use molecular data to examine 3 sub-species of parrot and hope to provide evidence for single species status for one of these birds along with

other morphological/distributional data they have collected. I would be grateful if anyone would provide comments or advise on any or the following queries that I have. I seem to remember that there can be some problems isolating mitochondrial from nuclear DNA during the extraction process. And that this may often be a problem with birds Are special extraction protocols required/recommended? With regard to species / sub-species discrimination: What length of bp is it recommended overall to sequence to enable species discrimination? Which are the most appropriate regions cytochrome b? is this best combined with another region/regions? Can anyone recommend primers that might be useful in parrots. Is there a recognised distance or percentage divergence that is accepted as appropriate for separating sub-species into species? Or what are the most appropriate techniques for this analysis? What number of individual birds are required to confirm consensus between individuals within each species/sub-species. Thanks for your help all comments and advice will be gratefully received. Tee Taylor

THE ANSWERS: ———————- my experience is not with birds but with a large group of closely related butterflies of which I have sequenced for mtDNA (COI) and nuclear DNA (ITS-2).

I do not think that nuclear pseudogenes (is that what you mean?) are a major problem if you work with standard primers, but I think that mtDNA analysis is not the appropriate method for your question.

Firstly, mtDNA gene trees often do not correspond to species trees in closely related species. (Therefore we have also included nuclear DNA.)

Secondly, although sometimes hidden species can be revealed through mtDNA analysis, there is NO recognized distance for species/subspecies divergence for good reason. From my experiences genetic distances between species can vary greatly. On the one hand we had well differentiated species in our analysis (which are different in phenotype, in karyotype and even occur sympatrically) which did not differ genetically in the markers used. On the other hand, some populations which are considered as belonging to the same species (and which do not differ in phenotype) can be genetically quite different. The problem is that mtDNA analysis cannot prove if gene flow persists or not, because you only have haplotypes. Microsatellite analysis would seem to be the more appropriate method for your question and even the good old allozymes seem preferable to mtDNA analysis.

Martin Wiemers

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i am not a bird person but what i can tell you is that you do not need to isolate mtDNA from the genomic DNA. if you just extract total DNA as you would do for microsats you can then use PCR to amplify specific regions of mtDNA. there's plenty of universal primers that have been published for vertebrates and i assume more specifically for birds.

Dr Andrea Verardi

> The group wish to use molecular data to examine 3 > sub-species of parrot and hope to provide evidence for single species > status for one of these birds along with other > morphological/distributional data they have collected.

Sounds like mtDNA will be a good component for this research.

> I seem to remember that there can be some > problems isolating mitochondrial from nuclear DNA during the extraction > process. And that this may often be a problem with birds

Yes, absolutely! This problem most often occurs with avian blood samples but can crop up from any tissue. If one works with feathers or

muscle tissue, nuclear copies of mtDNA are usually not a problem. Assuming that the parrots will be captured and released, I strongly recommend collecting feather samples (in addition to blood which may come in handy for future work on nuclear DNA). The feathers should be plucked, not cut, as the case of the quill (or calamus) if the part used for DNA extraction. From a parrot, one could pluck an inner secondary or a tail feather or even a couple of contour feathers from

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PostDocs

Cambridge ComputationalBiol

Research Associate in Computer Modelling of Prehistoric Populations

Applications are invited for the position of Research Associate in the Computer Modelling of Prehistoric Populations at the McDonald Institute, tenable for a period of two years. The primary duty of the research fellow will be to undertake computer simulations in population genetics. The successful candidate will have, or be expecting soon to obtain a PhD in a related topic, preferably within an anthropological or ecological environment. He or she should also be proficient in stochastic modelling, and ideally would be familiar with population genetics methods, including coalescent simulations and the role of computer simulations in anthropology. The person appointed will work in the Molecular Genetics Laboratory of the McDonald Institute for Archaeological Research, along with Dr Peter Forster and the person appointed to succeed Dr Matthew Hurles.

Salary will be on the scale £18,265 to £27,339 p.a. Applications with curriculum vitae and the names of two referees should be addressed to the Deputy Director, McDonald Institute for Archaeological Research, University of Cambridge, Downing Street, Cambridge CB2 3ER, United Kingdom (fax 44-1223-333536; tel. 333538, email dap38@cam.ac.uk) Closing date: 25th September 2003. Interviews will be held late October/early November.

Peter Forster <pf223@cam.ac.uk>

FloridaStateU ComputationalBiology

Open position for a postdoctoral associate.

I am looking for a person to collaborate in the field of population genetics, evolutionary epidemiology, bioinformatics. I hope to find someone that has skills in biostatistics, probability theory, theoretical population genetics, or theoretical evolution. If you have training/experience in some of the above and know a programming language (preferrably C or/and C++ and Mathematica), then send your CV, research interests, and the names, email addresses, and phone numbers of 3 people who know about you and your work to beerli@csit.fsu.edu [send it as plain text or as PDF files]. The postdoc position is for two years and starts this fall (or per agreement), projected salary is about $35,000 per year + health care benefits. I will make decisions after September 12, but the position remains open until filled.

I am interested in closely related species and population interactions and the inference of population parameters using maximum likelihood and Bayesian techniques (for more information see http://www.csit.fsu.edu/~beerli), and I am a member of the Computational Evolutionary Biology (CEB) group at Florida State University in Tallahassee. Other members of CEB are Mark Holder, Gavin Naylor (October 2003), Fredrik Ronquist (August 2003), Dave Swofford, Steve Thompson, Jim Wilgenbusch.

Peter Beerli —- School of Computational Science and Information Technology (CSIT) and Biology Department Dirac Science Library, Florida State University Tallahassee, Florida 32306-4120 USA Webpage: http://www.csit.fsu.edu/~beerli beerli@mac.com

LeidenU TheoBiol

Post-Doc position - Theoretical Biology, Leiden University (The Netherlands)

'Dimensions of Speciation'

We are looking for a Post-Doc to delve into certain aspects of models for the origin of new species. The simplified genetics in speciation models is often geared towards obtaining new species. In the allopatric case this is done by assuming certain relationships between fitnesses and genotypes. In the sympatric case this is done by only allowing the population to branch into two distinct phenotype classes through the development of assortative mating. In the allopatric case one can ask how an appropriate holey fitness landscape may develop through the interplay of a genotype to phenotype map and a population dynamics determining the density and frequency dependent fitnesses. In the sympatric case one can ask what happens when alternative mechanisms allowing for a phenotypic branching are present, like the availability of some developmental switch (e.g. based on an environmental cue, or on the presence or absence of a certain allele on a given major trait locus, or gender for that matter), with adaptive modification of the phenotypic effect of the switch. In particular one may ask the question what happens if different mechanisms are raced against each other.

In both cases the overall question is how the odds for certain outcomes depend on overall properties of the genetic architecture. The project should make a start with assessing the dependence of the odds for speciation on genetic and ecological degrees of freedom. The short term goal of the project is twofold: (1) Investigate the robustness of conclusions from existing speciation models by varying certain genetic and ecological dimensions. (2) Attempt to use the theory developed under (1) to analyse options for speciation in a model of a field system. This system should be often polymorphic, and in some cases this polymorphism should have resulted in the formation of separate species. A system of this type is found, for example, in butterfly mimicry rings.

The Leiden Theoretical Biology group offers a wide range of expertises. We i.a. specialise in adaptive dynamics, but other group members work on topics as diverse as RNA folding and phylogeny reconstruction. The work will be done in close collaboration with the Leiden Animal Ecology group. Between them the two groups offer the relevant experience and facilities.

Profile: PhD in Biology, Physics, Mathematics or Computer Science, preferentially with a specialization in Theoretical Biology. The appointment is for a maximum of two years. The gross monthly salary is between 2.136.= and 3.352,= euro, depending on prior experience. Salary and fringe benefits are conform the Collective Employment Agreement for Dutch Universities.

Further information and a project description can be obtained from:

Hans (= J.A.J.) Metz E-mail: metz@rulsfb.leidenuniv.nl group webpage with additional info: http://wwwbio.leidenuniv.nl/~eew/G8/index.html or Tom van Dooren E-mail: vdooren@rulsfb.leidenuniv.nl

Interested candidates should apply with a curriculum vitae, a covering letter and names and addresses of 3 potential referees.

MarylandCARB CompGeneEvol

Research Associateship in Computational & Statistical analysis of Gene Evolution

Qualified individuals are encouraged to apply for a post-doctoral Research Associateship at CARB*. The successful candidate will apply his or her expertise in statistical modeling and analysis to understanding the evolution of gene structure in eukaryotes, as part of an NIH-funded project on intron evolution (other team members are building the bioinformatics infrastructure to support large-scale analysis of gene evolution). More specifically, the successful candidate will develop methods to infer nucleotide sequence preferences for evolutionary intron gain, to predict features of the genic and genomic distribution of introns that arise from such preferences, and to test these predictions using available data. Opportunities exist for related research on gene and protein evolution.

Applicants must have Ph.D. in a relevant field, skill in computer programming, and research experience in statistical analysis and modeling, including familiarity

with ML and Bayesian inference. The position is a renewable one-year appointment (with probable renewal for 3 years), with a starting date in the fall of 2003, and with a yearly salary commensurate with experience.

To apply, send a cover letter, c.v., and contact information for three personal references to the address below. Review of applications will begin 25 August 2003 and will continue until the position is filled.

Dr. Arlin Stoltzfus (stoltzfu@umbi.umd.edu) Center for Advanced Research in Biotechnology 9600 Gudelsky Drive, Rockville, Md 20850 Tel: (301) 738-6208 Fax: (301) 738-6255

*The Center for Advanced Research in Biotechnology (www.carb.nist.gov) is a joint research center of the National Institute of Standards and Technology (NIST) and the University of Maryland Biotechnology Institute (UMBI). CARB is located in suburban Rockville, near Maryland's biotechnology corridor, and about 15 miles from Washington, DC. Basic research at CARB is both theoretical and experimental, and focuses on macromolecular structure and function. CARB is an EEO/AA Employer. Women and minority candidates are especially encouraged to apply.

NorthCarolinaStateU MosquitoEvolution

MICROBIAL/CHEMICAL ECOLOGY POST-DOCTORAL RESEARCH ASSOCIATE

Applications are invited for a post-doctoral research associate position, available immediately, to investigate bacterially-derived semiochemicals that mediate mosquito oviposition behavior. This is a collaborative project between the Apperson and Schal labs. The postdoc will isolate microbes that produce metabolites that mediate the oviposition responses of mosquitoes, identify bacteria using molecular techniques, conduct behavioral assays to determine which bacterial species or combinations of species produce attractants or stimulants that are active against gravid mosquitoes, identify the chemicals produced by these species, verify the activity of putative oviposition attractants in dose-response behavioral bioassays against laboratory populations, test the compounds individually and in mixtures, and develop optimal mixtures of oviposition chemicals to be formulated into controlled release lures, which will be field-tested to determine if the lure enhances the activity of oviposition traps used for surveillance of populations of mosquitoes.

Qualifications: Ph.D. trained in microbiology, entomology, or related fields. Experience in microbial ecology, including culture and identification of bacterial species. Alternatively, chemical ecology, including extraction, purification, behavioral assays and identification of semiochemicals. Instrumentation skills, including GC, MS, TLC, HPLC, and electrophysiology (EAG, GC-EAD) experience desirable.

APPLICATION: Submit curriculum vitae, relevant reprints and manuscripts, letter describing background, skills and interests. Also submit names, addresses and phone numbers of three references to:

Coby Schal Department of Entomology Box 7613 North Carolina State University Raleigh, North Carolina 27695-7613 tel. 919.515.1821 coby_schal@ncsu.edu

SangerInst GenomeEvol

Post-Doctoral Research Associates

The Wellcome Trust Sanger Institute is a world leader in genome science. The Genome Dynamics and Evolution group within the institute is dedicated to improving our understanding of interactions between duplicated sequences within the human genome. Our objectives are to provide insights into fundamental pathogenic mechanisms and reveal novel processes of evolutionary change.

To further these exciting research goals we are looking for two highly motivated scientists who are keen to learn and develop new technologies and have the ability to work independently while being part of a team. These will be varied roles with opportunities to work on a range of projects.

Evolution of segmental duplications - evol-662

The post-holder will primarily be engaged in projects to investigate sequence variation and haplotype diversity in and around segmental duplications in the human genome. The applicant should have a Ph.D. in molecular genetics and be familiar with DNA sequence assembly tools and molecular evolutionary analyses. Knowledge of human population genetics would be an advantage.

Dynamics of chromosomal rearrangements - evol-663

The post-holder will primarily be engaged in the development of efficient methods to detect chromosomal rearrangements. The applicant should have a Ph.D. in molecular genetics and be familiar with PCR-based methods such as SNP typing, multiplex PCR or single-molecule PCR. Experience of developing novel methodologies would be an advantage.

For further information see http://www.sanger.ac.uk/-Teams/Team29/ <http://www.sanger.ac.uk/-Teams/Team29/> ,informal enquiries should be directed to Matt Hurles meh@sanger.ac.uk <mailto:meh@sanger.ac.uk>

To apply for these positions, please send a full CV including a list of publications, current salary details, and the names and addresses of three referees, together with a covering letter quoting the appropriate reference number to:

Human Resources, Wellcome Trust Sanger Institute, Hinxton, Cambridge, CB10 1SA.

Or email your application to humanresources@sanger.ac.uk <mailto:humanresources@sanger.ac.uk>

The closing date for applications is 19th September 2003

www.sanger.ac.uk

Sarah Golland Human Resources Officer

Genome Research Limited The Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SA

Tel: 01223 494943 fax: 01223 494859 http://-www.sanger.ac.uk <http://www.sanger.ac.uk

Sarah Golland <skg@sanger.ac.uk>

UAlaskaFairbanks PlantGenet

POSTDOCTORAL POSITION IN PLANT ECOLOGICAL GENETICS AT

THE UNIVERSITY OF ALASKA AT FAIRBANKS

DEPARTMENT: Institute of Arctic Biology

JOB TITLE: Post Doctoral Fellow

PCN#: 924214

REQ NUMBER: FF92421401

OPENING DATE: July 29, 2003

CLOSING DATE: August 5, 2003

An NSF-funded postdoctoral position is available to study the fitness consequences of genes controlling sex expression in Silene vulgaris, a gynodioecious plant with cytoplasmic male sterility. The goal of the project will be to perform a rigorous experimental test for the cost of restoration on 3 CMS/restorer systems that have been identified through marker and crossing studies. The research will provide a deeper understanding of the maintenance and resolution of the selective interests of cytoplasmic and nuclear genes in gynodioecious plants. The results will help provide a framework with which to interpret issues such as the interactions between cytoplasmic diseases and autosomal resistance genes and the evolution of complex genetic sex determination and transmission systems. Further information on this study system can be found in:

Olson, M.S. and D.E. McCauley. 2002. Mitochondrial DNA diversity, population structure, and gender association in the gynodioecious plant Silene vulgaris. Evolution, 56: 253-262.

The position will involve greenhouse crossing studies, field experiments, and molecular marker screening in the laboratory. Opportunities will be available to participate in and develop additional crossing, molecular, and/or theoretical projects related to the overall goals of this study. The successful applicant will interact with an active group of faculty, postdocs, and graduate students at the Institute of Arctic Biology <http://mercury.bio.uaf.edu/iab/index.html>http://-mercury.bio.uaf.edu/iab/index.html.

Candidates should have a strong background in population genetics and an earned Ph.D. Candidates with molecular experience are encouraged to apply. Salary range will vary from $32,000-37,000 depending on experience and includes a benefits package. The opening date for this posotion is August 15, 2003. The position is open until filled and review of applications will begin on August 29, 2003. To obtain further information about the position please contact Matt Olson by email (<mailto:matt.olson@uaf.edu>matt.olson@uaf.edu).

APPLICATION: We do not accept application materials via email. Please follow specific instructions provided on each vacancy announcement. Applicants must submit a separate application packet for each position. All application packets must include:

<http://www.alaska.edu/hr/forms/PDF_ent/-applicant_form.pdf>UA Applicant Form - mandatory when applying for any UAF position. A separate Applicant Form is required for each position for which you apply.

Professional resume, curriculum vitae. The <http://www.alaska.edu/hr/forms/PDF_ent/-resume_form_ent.pdf>Resume Form may be used as a substitute for resume.

The names, addresses, telephone numbers of three (3) professional references. For faculty positions you must provide three (3) professional letters of reference.

Please submit application packet to:

UAF Human Resources c/o Marta Conner 3295 College Road, Room 108 PO Box 757860 Fairbanks, Alaska 99775-7860

Phone: (907) 474-7700 Fax: (907) 474-5859

All required materials must be received by 4:30 p.m. on or before the closing date. If you choose to fax your application packet, you must transmit by 4:00 p.m. Alaska Standard Time (AST) on or before the closing date to ensure consideration of employment.

ALL APPLICANTS THAT DO NOT SUBMIT THEIR APPLICATION PACKETS TO UAF HUMAN RESOURCES WILL BE ELIMINATED FROM FURTHER CONSIDERATION.

All finalists may be subject to a background check

Matt Olson <matt.olson@uaf.edu>

UBritishColumbia PopulationGenomics

Post-doctoral position Population genomics University of British Columbia Vancouver, Canada

A post-doctoral position is open in the laboratory of Kermit Ritland to investigate questions in theoretical and/or statistical aspects of genome evolution in populations. Background in population or evolutionary genetics, knowledge of some statistics, and evidence of programming ability, are essential. The type of research depends upon your background and interests, but may include activities such as inferences about selection based upon SNP variation, patterns of multilocus evolution, or association studies. The types of questions could be highly aligned with the data emerging from the Forestry Genome BC project (www.genomebc.ca) currently underway in our department (Forest Sciences), and with other genome projects. At the University of British Columbia, there are several other research groups in population and evolutionary genetics, including those of Dolph Schulter, Sally Otto, Mike Whitlock and Quentin Cronk. Vancouver is also well-known for its environment and lifestyle. The position is funded mostly by NSERC of Canada, for ca. 35K (CAN) per year for two years, and is available immediately. Submit applications to: Kermit.Ritland@ubc.ca.

UCDavis TransposableElements

UNIVERSITY OF CALIFORNIA Post-Doctoral Position

Post doc to work on genomics / population genetics of transposable elements in the lab of Sergey Nuzhdin, Evolution and Ecology, University of California at Davis (and possibly another one to work on quantitative genetics of expression variation, 3 years, $31K, one starting now, another in November/December). Our pop. / quant. genetics / evolution crowd is a very fun place to be at. On the same floor, there are labs of Begun, Gillespie, Langley, Turelli, and mine with joint discussion groups and lots of cross-lab interactions. A postdoc might expect demanding scientific environment combined with lots of academic freedom. Please, inquire at svnuzhdin@ucdavis.edu.

UCopenhagen Insects

"INSECTS" POSTDOCTORAL FELLOWSHIP, UNIVERSITY OF COPENHAGEN

Prof. Koos Boomsma's group at the University of Copenhagen is seeking a postdoc to be employed as part of the EU "INSECTS" network for a one-year fellowship to start in Autumn 2003 and no later than 1 January 2004.

More details of the INSECTS network can be found at:

http://www.zi.ku.dk/eunet/ The Copenhagen group currently has active research programs examining population genetics of invasive ants, coevolution of fungus-growing ants and termites and their symbiotic fungi, the evolution of multiple-mating, worker policing in attine ants, the evolution of social parasites of ants, and the evolution of chemical and social defences against parasites. Model organisms used include

fungus-growing ants (Attini), fungus-growing termites (Macrotermitinae), invasive and parasitic Lasius ants, pharoah's ants, bumblebees and lycaenid butterflies. The group is also very active in collaborations with other INSECTS partners.

We are seeking a postdoc who will fit in with the general interests of the group, but who will conduct independent research. The successful candidate will also be affiliated with the Centre for Social Evolution and Symbiosis in Copenhagen.

More information about the research carried out in the group can be found at the following sites:

Koos Boomsma's personal home page: http://-www.zi.ku.dk/personal/jjboomsma/mainpage.htm Centre for Social Evolution and Symbiosis: http:/-/www.zi.ku.dk/cses/ Research on ant symbioses at Copenhagen: http://www.zi.ku.dk/personal/drnash/-atta/default.htm Candidates who are interested in the position, and who meet the eligibility requirements (European citizenship, aged under 35 - Full details available from the INSECTS web site), are encouraged to contact Koos Boomsma (JJBoomsma@zi.ku.dk) as soon as possible.

UDublin BeeGenetics

A postdoc and a PhD position in conservation and population genetics

Conservation genetics of Irish bees - a whole island perspective, funded by the HEA North South Programme for Collaborative Research Strand 1, is a collaboration between Dr Mark Brown (University of Dublin Trinity College, http://www.tcd.ie/Zoology/text/brown.htm) and Dr Robert Paxton (Queen's University Belfast, http://www.qub.ac.uk/bb/). We are looking for:

1) a post-doctoral researcher, to be based in Dublin. You must have skills and experience in population and/or conservation genetics, especially with respect to the use of microsatellite analysis. It would be helpful if you had experience in insect field work and/or the application of GIS techniques to species distribution data. Duration: 3 years, on the equivalent of the UK post-doctoral pay scale RA1A (circa Euro 30,000 p.a., depending on age and experience). No nationality restrictions.

2) a PhD student, to be based in Belfast. Experience in molecular genetic techniques, and an interest in insects, conservation and field biology would be helpful. Duration: 3 year, with a PhD stipend (circa GBP 10,500 p.a.); no nationality restrictions, though non-EU nationals will need to pay overseas postgraduate fees.

The successful applicants will (i) conduct basic fieldwork to determine baseline data on the distribution and abundance of solitary, semi- and eusocial bee species, (ii) develop and apply microsatellite markers to determine the population and conservation genetic status of these species, and (iii) develop a GIS-based database for the Irish bee fauna. Training can be provided in all of these areas if necessary, depending upon the applicant. Public outreach and integration between the two collaborating labs are important parts of the programme.

While there is no final date for applications, we seek to employ applicants for the 2003-2004 academic year (start 6 October 2003, though some flexibility about starting dates exists).

For further information, please contact either Dr Mark Brown (mabrown@tcd.ie) or Dr Rob Paxton (r.paxton@qub.ac.uk).

Robert John Paxton <r.paxton@qub.ac.uk>

UFerraraIT PopGenet

Post-doctoral position in Population Genetics University of Ferrara, Italy

A one-year post-doctoral position, renewable for a second year, is available in Guido Barbujani's laboratory to investigate questions in population genetics and molecular evolution. The specific research projects will depend on the successful candidate's interests, but have to do with the analysis of population genetic data for the reconstruction of past demographic processes and selection events. For more information on the personnel and the activities of the lab, check this website: <http://web.unife.it/progetti/genetica/>http:/-/web.unife.it/progetti/genetic a/. Candidates with a strong background in population genetics and biostatistics, and who are familiar with standard computer packages for genetic data analysis, are encouraged to apply. Programming skills are a plus.

The position, funded by the University of Ferrara and by the FISR programme

of the Italian Ministry for the Universities, will be avail-

able starting January 2004, or when a suitable candidate will emerge. Net salary (after taxes) is 15,000 per year, and full health insurance (for foreign candidates) is 150 per year.

Submit a curriculum vitae and two letters of recommendation to: G.Barbujani@unife.it.

Guido Barbujani Dipartimento di Biologia, Università di Ferrara via L. Borsari 46, I-44100 Ferrara, Italia Phone: +39 0532 291312 Fax: +39 0532 249761 webpage: http://web.unife.it/progetti/genetica/Guido/-Guido.html=20

UMichigan Phylogeography

University of Michigan: Postdoctoral in Plant and Insect Phylogeography

Applications are solicited for a one-year postdoctoral position in the Department of Ecology and Evolutionary Biology at the University of Michigan, for analysis of the phylogeography of plants and associated host-specific insects. Proficiency with methods of obtaining sequence and microsatellite data, experience with phylogeographic or phylogenetic analysis, and a background in evolutionary biology are expected. Aid in learning methods specific for either plant or insect material is available if needed. The successful applicant will help to complete the setup of a new lab. The salary level will be $28,000 per year. The position will start as soon as a suitable candidate can arrive.

Applicants should send a curriculum vitae, statement of research interests, and publications or manuscripts, and arrange to have three letters of recommendation sent to Douglas Futuyma, Dept. of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI 48109-1048; or email dfutuyma@umich.edu. Applications will be accepted until a suitable candidate is found. The University of Michigan is a nondiscriminatory affirmative-action employer.

Douglas J. Futuyma Professor Department of Ecology and Evolutionary Biology University of Michigan Natural Science Building 830 North University Avenue Ann Arbor, MI 48109-1048

tel. (734) 936-0549 fax (734) 763-0544 dfutuyma@umich.edu

UNotreDame SpeciesBoundaries

POSTDOCTORAL POSITION University of Notre Dame

POPULATION GENETICS OF SPECIES' RANGE BOUNDARIES A postdoctoral research position is available in the Hellmann Lab (Department of Biological Sciences, University of Notre Dame) to study the genetics of populations at their northern range limit. I am looking for someone well-versed in molecular techniques who is interested in bringing genetic studies to bear on issues of global change and applied ecology. The position is to join a multi-faceted research project examining both the ecological and evolutionary impacts of climate change on the distributional limits of two model butterflies species. This research grows out of previous studies by Dr. Hellmann on the impacts of climate change in grassland ecosystems (for example, see: Hellmann, J. 2002. J An Ecol 70:925-936; McLaughlin, J., Hellmann, J., Boggs, C., and P. Ehrlich. 2002. PNAS 99:6070-6074). Our current research examines the hypothesis that differences in life history traits lead to distinct patterns of gene flow across a species' range and that taxa with contrasting genetic structures will respond differently to climatic warming. Mechanistic studies of species' range shifts are an emerging area of global change biology that is highly policy-relevant. This position offers an opportunity for a geneticist to join ecologists in tackling this novel area of applied research.

The successful candidate must demonstrate an intellectual commitment to research in applied biology and is expected to pursue both independent research and molecular assessments of gene flow. Marker development for this project will build on systematic and evolutionary work pursued by other lepidopteran researchers. Exactly which markers and techniques will be used will depend on the mutual interests of the successful candidate and the PI. The position has guaranteed funding for two years. Resources available in the pursuit of this research include a strong molecular genetics faculty within the biology department at Notre Dame.

This position is open until filled. Salary is commensurate with experience. Applicants should send a brief letter describing their prior research experience and current interests, a curriculum vitae, and the names and contact information of three references to: Jessica

Hellmann, Assistant Professor, Department of Biological Sciences, 107 Galvin Life Science Center, University of Notre Dame, Notre Dame, IN 46556 (fax: 574-631-7413; email: hellmann.3@nd.edu).

The University of Notre Dame is an Equal Opportunity/Affirmative Action Employer.

---------- Jessica J. Hellmann Assistant Professor Dept. of Biol. Sciences University of Notre Dame (574) 631-7521 hellmann.3@nd.edu ----------

UNottingham EvolDevol

Institute of Genetics, University of Nottingham, UK

Post-Doctoral Research Associate

Research in Drosophila Developmental and Evolutionary Genetics

A post-doctoral research associate is sought by Dr. J.F.Y. Brookfield at the Institute of Genetics, University of Nottingham, to work on a three-year BBSRC-funded project examining the microevolution of development in Drosophila. The work will involve experimental manipulation of enhancer sequences from flies of the D. melanogaster species group, and their introduction into D. melanogaster. We are seeking a researcher with experience in genetic manipulation, ideally in the context of Drosophila, and with a strong interest in evolution.

The starting salary will be in the range of £18265 - 200311 pa. depending on qualifications and experience. This post will be offered on a fixed-term contract for a period of three years, starting as soon as possible after the 1st October 2003.

For further information, contact J.F.Y. Brookfield, Tel: (44)-(0)115-970-9401, email john.brookfield@nottingham.ac.uk.

Candidates should send a detailed CV, together with the names and addresses of two referees, to Dr J.F.Y.Brookfield, Institute of Genetics, Queen's Medical Centre, Nottingham, NG7 2UH. Closing date: 22nd August 2003.

John Brookfield <John.Brookfield@nottingham.ac.uk>

UOxford ViralEvol

POSTDOC IN VIRAL EVOLUTION,

DEPARTMENT OF ZOOLOGY, UNIVERSITY OF OXFORD

Postdoctoral Research Assistant,

Academic-Related Research Staff Grade 1A: Salary range: £18,265 - £27,339 p.a.

Applications are invited for a postdoctoral research assistant, funded by the Wellcome Trust, to work on the evolutionary genetics of RNA viruses. The project represents a collaboration between Dr. Eddie Holmes, University of Oxford, and Dr. Andrés Moya, University of Valencia, and will combine both phylogenetic and experimental approaches to the study of RNA virus evolution. This postdoctoral position will involve large-scale phylogenetic and population genetic analyses of a wide range of RNA viruses and will be based in the Department of Zoology, Oxford. Experience in phylogenetics and computer programming are highly desirable. This position will run for 3 years and will start as soon as possible after the 1st October 2003.

Further particulars are available from Sally.Burton@zoo.ox.ac.uk. Applications should be addressed to the Administrator, Department of Zoology, Tinbergen Building, South Parks Road, Oxford OX1 3PS, enclosing contact details of three referees and quoting reference: AT03028. Informal enquiries to Dr. Eddie Holmes, e-mail: Edward.Holmes@zoo.ox.ac.uk (I am away until August 29th, so please do not expect a speedy response). The closing date for applications is Monday 8th September 2003.

Eddie Holmes <edward.holmes@zoology.oxford.ac.uk>
Eddie Holmes <edward.holmes@zoology.oxford.ac.uk>

UWaterloo PlantMicroarrays

POSITIONS AVAILABLE: POSTDOCTORAL FELLOWS

We are seeking highly motivated individuals to work on

a microarray project to examine patterns of gene expression in response to abiotic stress (freezing, drought and high salinity) in an Arctic crucifer that is closely related to Arabidopsis, but is far more stress-tolerant than Arabidopsis. The project is directed by four faculty members at the University of Waterloo and McMaster University: Dr. Barbara Moffatt (plant molecular genetics), Dr. Marilyn Griffith (physiology of freezing tolerance), Dr. Elizabeth Weretilnyk (physiology of salt and drought tolerance), and Dr. Brian Golding (bioinformatics). Applicants should have proven research skills in genetic, molecular and cellular biology and ideally should include significant research experience in the following techniques: RNA isolation; PCR; examination of gene expression by northern analysis and RT-PCR, in situ hybridization; transformation and gene silencing; and protein overexpression. These positions require excellent communication and organizational skills and are available immediately. Applicants should have a PhD degree and relevant research experience. These are two-year positions, both with a competitive salary (plus benefits). Interested candidates should send a cover letter outlining research experience and interests, a curriculum vitae including names and phone numbers of three referees to Dr. Barbara Moffatt, Department of Biology, University of Waterloo, Waterloo, ON, N2L 3G1, Canada, moffatt@sciborg.uwaterloo.ca, telephone: 519-888-4567 ext. 2517, FAX: 519-746-0614. University of Waterloo hires on the basis of merit and is committed to employment equity. The positions will remain open until suitable candidates are found.

Dr. Marilyn Griffith Department of Biology, University of Waterloo 200 University Avenue West Waterloo, ON N2L 3G1 Canada Tel 519-888-4567 ext 6441 FAX 519-746-0614 griffith@uwaterloo.ca

VanderbiltU SunflowerEvol

An NSF-funded postdoctoral position is available in the Burke lab at Vanderbilt University. The goal of this project is to identify and characterize genes that were under selection during the domestication of sunflower. This work will combine genotypic and sequence-based approaches to identify genes bearing the population genetic signature of selection. The functionality of such genes will then be investigated by genetically mapping them and comparing their genomic locations to those of QTLs underlying domestication traits, as well as through analyses of gene expression. Background information can be found in:

Burke, J.M., S. Tang, S.J. Knapp, and L.H. Rieseberg. 2002. Genetic analysis of sunflower domestication. Genetics 161: 1257-1267.

This research provides an ideal opportunity for applicants interested in the molecular basis of phenotypic evolution. Funding is available for up to five (5) years and, although the position is available immediately, the start data is flexible. Candidates should have a strong background in population genetics with experience applying molecular tools to evolutionary questions.

To apply, please send your CV, a brief statement of research interests, and letters from three references to:

John M. Burke, PhD Vanderbilt University Department of Biological Sciences VU Station B 351634 Nashville, TN 37221

or (preferably) via e-mail to: john.m.burke@vanderbilt.edu

For more information about the Vanderbilt University Department of Biological Sciences, please visit:

http://sitemason.vanderbilt.edu/biosci/ Information on the Burke lab can be found at:

http://www.biosci.vanderbilt.edu/mbdept/faculty/-burke.html –

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John M. Burke, Ph.D. Tel: 615.936.3892 Fax: 615.343.6707

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Vanderbilt University Department of Biological Sciences VU Station B 351634 Nashville, TN 37235

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Courier Address (e.g., FedEx, UPS): 7268 Biological Sciences/MRB III 465 21st Avenue South Nashville, TN 37232

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WashingtonU EvolGenet

A postdoctoral research position is available for work in evolutionary population genetics. The position is aimed at two target audiences: The first is someone with a PhD in biology or genetics or a related field, who has some experience in statistics and numerical computation, and who would like to learn more by

working on one or more projects in this area. A typical candidate would be someone with some statistical and programming knowledge who would like to learn more about modern maximum likelihood and/or MCMC techniques. The second target audience would be composed of people with a background in a quantitative field such as mathematics, statistics, or physics and who would like to learn about applying these techniques to mathematical or evolutionary genetics. In either case, the candidate should be familiar with a procedural language such as C or one of its friends (C++ or Java) or else Fortran or Pascal (or etc.) and be willing to work in one of C/C++/Java.

The position is supported by an NSF grant whose aim is to work on methods for inferring quantitative estimates of selection from aligned DNA sequences. However, the candidate will have considerable freedom in choice of topics.

The position is available from Oct 1, 2003, and will remain open until the best candidate is found. The salary will be $35,000 per year plus benefits. The initial appointment will be for one year with a likelihood of extension for a second year or longer subject to availability of grant funds. (The grant now has funds for two years.) Candidates should send an email letter to Stanley Sawyer at the email address below with a statements of research interests and of their research background, a curriculum vitae, and the names and email addresses of three references. Women and minorities are particularly encouraged to apply.

Some typical relevant references for Stanley Sawyer (see Web site for others) are:

Sawyer, S. A. (1994) Inferring selection and mutation from DNA sequences: The McDonald-Kreitman test revisited. In G. B. Golding (Ed.) Non-Neutral Evolution: Theories and Molecular Data. Chapman & Hall, New York, 77-87.

Sawyer, S. A. and D. L. Hartl (1992) Population genetics of polymorphism and divergence. Genetics 132, 1161-1176.

Bustamante, Carlos, Rasmus Nielsen, Stanley A. Sawyer, Kenneth M. Olsen, Michael D. Purugganan, and Daniel L. Hartl (2002) The cost of inbreeding in Arabidopsis. Nature 416, 531-534.

Sawyer, Stanley A, Rob J. Kulathinal, Carlos D. Bustamante, and Daniel L. Hartl (2003) Bayesian analysis suggests that most amino acid replacements in Drosophila are driven by positive selection. In press.

Bustamante, Carlos D., John Wakeley, Stanley Sawyer, and Daniel L. Hartl (2001) Directional selection and the site-frequency spectrum. Genetics 159, 1779-1788.

Padidam, Malla, Stanley Sawyer, and Claude M. Fauquet (1999) Possible emergence of new geminiviruses by frequent recombination. Virology 265, 218-225.

Sawyer, S. A. (1989) Statistical tests for detecting gene conversion. Molecular Biology and Evolution 6, 526-538.

Sawyer, S. A. (1990) Maximum likelihood estimators for incorrect models, with an application to ascertainment bias for continuous characters. Theoretical Population Biology 38, 351-366.

Stanley Sawyer Professor of Mathematics, Genetics, and Biostatistics Department of Mathematics Washington University St.Louis, MO 63130 email: sawyer@math.wustl.edu Voice: 314-935-6703 FAX: 314-935-6839 (Mathematics department) Web: http:/-/www.math.wustl.edu/ sawyer

WashingtonU EvolGenetics

POSTDOCTORAL POSITION EVOLUTIONARY GENETICS

A postdoctoral position in evolutionary genetics is available in the genetics department of Washington University. The project involves relating sequence variation to variation in gene expression and to phenotypic variation found among natural isolates of Saccharomyces cerevisiae. Expression differences have already been associated with phenotypic differences. The segregation of these expression differences with markers and phenotypes will be used to understand the contribution of gene expression to complex traits. Yeast genome technologies will be used to rapidly map quantitative characters. Applicants should have a strong background in either molecular biology, evolutionary biology or computational biology.

The salary is 45K and funds are available for three years. Applicants should send a CV and the names and numbers of two references to Justin Fay <jfay@genetics.wustl.edu>

Justin Fay Assistant Professor of Genetics Washington University School of Medicine 4566 Scott Ave, St. Louis, MO 63110 PH: 314.747.1808 Fax: 314.362.7855

Justin Fay <jfay@genetics.wustl.edu>

WorkshopsCourses

MBL MolEvol URL

Dear Colleagues,

The Web site for the Workshop on Molecular Evolution has moved. The new address is http://-workshop.molecularevolution.org .

cheers,

Mike

– Michael P. Cummings Center for Bioinformatics and Computational Biology University of Maryland Agri/LFSc Surge Building #296 College Park, MD 20742-3360 USA mike@umiacs.umd.edu 301.405.9903 voice 301.314.1341 facsimile http://-serine.umiacs.umd.edu/

UArizona Drsophila Oct29-Nov2

Drosophila Species Workshop III October 29 to November 2, 2003 University of Arizona Tucson, Arizona

REGISTRATION FORM Registration Deadline: September 19, 2003

Return form with payment to: Drosophila Species Workshop III Center for Insect Science University of Arizona P.O. Box 210106 Tucson, Arizona 85721-0106

Name

Title

Mailing Address

City State/Province

Zip/Postal Code Country

Telephone FAX Email

Registration Information

The registration fee includes all instruction, instructional materials, rec eption and dinner. Among the instructors will be Wyatt Anderson, Universit y of Georgia, William Heed and Therese Markow, University of Arizona, Bryan t McAllister, University of Iowa, Patrick O'Grady, University of Vermont an d Marshall Wheeler, Emeritus, University of Austin. The species groups to be covered are the D. melanogaster, D. obscura, D. virilis, and D. repleta.

Registration Fee US $300.00

Method of Payment Check made payable to the University of Arizona

Cancellations Registration fees will not be refunded for cancellations rece ived after the registration deadline of September 19, 2003.

Questions Contact Sharon Richards, insects@arl.arizona.edu, 520-621-9310

Third Annual Drosophila Species Workshop October 29 to November 2, 2003 University of Arizona Research Labs

The Tucson Drosophila Species Stock Center will hold a four day workshop fo r 14 investigators interested in learning to identify different Drosophila species, collect flies in nature, prepare culture medium for species with d ifferent dietary requirements and become familiar with culture techniques n ecessary to successfully utilize non-melanogaster Drosophila species in the ir research. Instruction will take place on Thursday, Friday,

Saturday and Sunday. Participants should plan to arrive in Tucson by Wednesday evening , October 29 and leave no earlier than late Sunday afternoon, November 2. The $300 registration fee will include all instruction, instructional mater ials, Friday evening reception, Saturday evening dinner. The Center for In sect Science will assist students with limited funds in finding housing wit h UA graduate students. For additional information please contact: Sharon Richards, Program Coordinator, Center for insect Science, University of Ar izona at insects@arl.arizona.edu.

Among the instructors will be Wyatt Anderson University of Georgia, William Heed and Therese Markow, University of Arizona, Bryant McAllister, Univers ity of Iowa, Patrick O'Grady, University of Vermont and Marshall Wheeler, E meritus, University of Austin. The 2003 workshop will cover the D. melanog aster, D. obscura, D. virilis, and D. repleta species groups.

Lisa Andrus <lgandrus@email.arizona.edu>

UHawaii EvolComp

On-line course offering: ICS 691: Evolutionary Computation (Topics in Software), Department of Information and Computer Sciences, University of Hawaii at Manoa.

There are a number of seats available through the Outreach College at the University of Hawaii at Manoa for the on-line graduate level course in evolutionary computation that I am offering for this semester. This course will be an introduction to the field of evolutionary computation (genetic algorithms, evolution strategies, evolutionary programming, genetic programming, artificial life), geared to getting the student involved in research in the field as quickly as possible. Course work will consist of a research project, class discussions, and readings from the texts:

Evolutionary Computation 1: Basic Algorithms and Operators , ed. T. Back, D. B. Fogel and T. Michalewicz, Institute of Physics Publishing, Bristol and Philadelphia. ISBN 0-7503-0664-5. 2000.

Evolutionary Computation 2: Advanced Algorithms and Operators , ed. T. Back, D. B. Fogel and T. Michalewicz, Institute of Physics Publishing, Bristol and Philadelphia. ISBN 0-7503-0665-3. 2000.

Research projects can be on applications, theory, history, or empirical studies of evolutionary algorithms. The goal is that the student's project be published in one of the many proceedings or journals on evolutionary computation. The course is entirely Web-based, using the Blackboard system, and asynchronous, except for deadlines on submissions.

This fall's introductory course will be followed in the Spring 2004 semester by an in-depth course on Genetic Programming, which is the application of evolutionary approaches to the engineering of executable programs.

Registration information is available at http://www.outreach.hawaii.edu/registration/-apply_register.html Additional information is available at my Web site,

http://dynamics.org/Altenberg/UH_ICS/ The course begins August 25, but registration is still possible after that date.

Questions about the course can be e-mailed to me directly. Best regards, Dr. Lee Altenberg

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Lee Altenberg, Ph.D. Associate Professor, Information and Computer Sciences University of Hawai'i at Manoa Phone: (808) 875-0745, Fax: call to arrange E-mail: altenber@hawaii.edu, altenber@santafe.edu Web: http:/-/dynamics.org/Altenberg/

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject

heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. ... plain old ASCII will work great and can be read by everyone. Add a subject header that contains one of the keywords "Conference, Grad, Job, Other:, Postdoc, Workshop" and then the message stands a better chance of being correctly parsed.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. So please do not expect an instant response.

Afterward

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.